



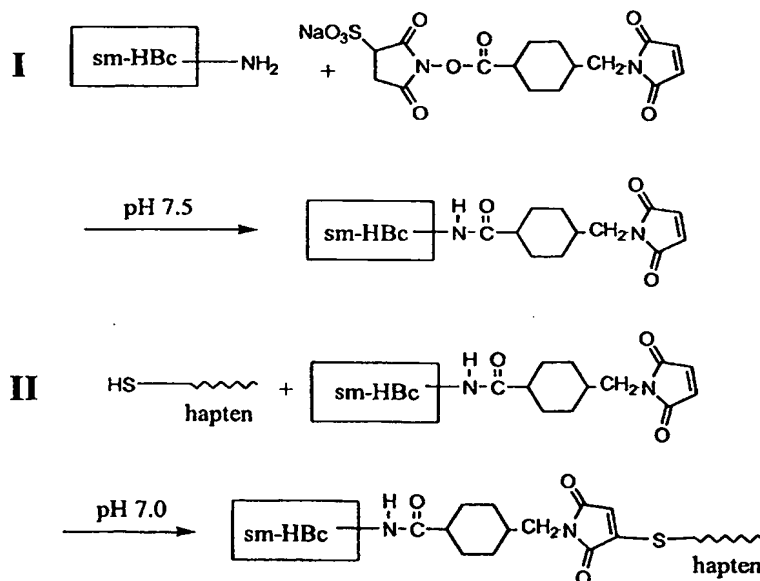
PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification <sup>6</sup> : A61K 39/00, 39/38, 39/29, C07K 7/00, 15/00</p>	<p>A1</p>	<p>(11) International Publication Number: <b>WO 99/40934</b> (43) International Publication Date: 19 August 1999 (19.08.99)</p>
<p>(21) International Application Number: PCT/US99/03055 (22) International Filing Date: 11 February 1999 (11.02.99) (30) Priority Data: 60/074,537 12 February 1998 (12.02.98) US (71) Applicant: IMMUNE COMPLEX, CORPORATION [US/US]; 3347 Industrial Court, San Diego, CA 92121 (US). (72) Inventor: BIRKETT, Ashley, J.; Apartment 3208, 878 Stevens Avenue, Solana Beach, CA 92075 (US). (74) Agents: GAMSON, Edward, P. et al.; Welsh &amp; Katz, Ltd., 22nd floor, 120 South Riverside Plaza, Chicago, IL 60606 (US).</p>	<p>(81) Designated States: AL, AU, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GE, HU, ID, IL, IS, JP, KP, KR, LC, LK, LR, LT, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SD, SG, SI, SK, SL, TR, TT, UA, UZ, VN, YU, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> <i>With international search report.</i></p>	

(54) Title: STRATEGICALLY MODIFIED HEPATITIS B CORE PROTEINS AND THEIR DERIVATIVES



(57) Abstract

A strategically modified hepatitis B core protein is described, where an insert is provided, preferably in an immunodominant region of the nucleocapsid protein, containing a chemically reactive amino acid residue. The modified hepatitis B core protein or its aggregated nucleocapsid protein particles can be pendently linked to a hapten to form a modified nucleocapsid conjugate. Such a conjugate is useful in the preparation of vaccines or antibodies. The modified hepatitis B core protein can also be modified to include a T cell epitope.

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CJ	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

STRATEGICALLY MODIFIED HEPATITIS B CORE  
PROTEINS AND THEIR DERIVATIVES

Description

5

Technical Field

The present invention relates to the intersection of the fields of immunology and protein engineering, and particularly to carrier proteins, and more particularly to a hepadnavirus nucleocapsid protein strategically modified with an inserted chemically-reactive amino acid residue, a pendently-linked hapten conjugate of that hepadnavirus nucleocapsid protein and to an immunogenic particle comprised of those conjugates.

15

Background of the Invention

It is known that antibodies can be raised to a small molecule by using a large immunogenic protein molecule as a carrier. The small molecule that derives enhanced immunogenicity by being conjugated to the carrier is called a hapten. The phenomenon of a relatively large molecule potentiating the immunogenicity of a small molecular entity to which it is attached is known in the art as the "carrier effect".

20

25

The portion of an immunogen recognized by the helper T cell (Th cell) is the T cell determinant or epitope. The portion of an immunogen that is bound by antibody is the B cell determinant or epitope. Carrier effects can be defined as immunity to one determinant, the "helper" or T (T<sub>h</sub>) cell

30

-2-

determinant, of a multideterminant immunogen enhancing the immune response to another determinant, the B cell determinant.

It is now well established that most  
5 immunogens require T cell help to induce B cells to produce antibodies. Thus,  $T_h$  cells, by recognizing helper determinants on the immunogen help B cells to make antibody against the immunogen.

The antigenic determinants recognized by T  
10 helper cells ( $T_h$ ) and B cells must be associated to form a single molecular entity, but they do not have to be covalently linked. See, Russel et al., *Nature*, 280:147 (1979), Lamb et al., *J. Immunol.*, 129:1465 (1982), Scherle et al., *J. Exp. Med.*, 164:1114 (1986)  
15 and Lake et al., *Cold Spring Harbor Symp. Quant. Biol.*, 41:589 (1976). Some immunogens do not require T cell help to induce antibody formation, these are T-independent antigens.

A pathogen-related protein can be  
20 immunologically mimicked by the production of a synthetic polypeptide whose sequence corresponds to that of a determinant of the pathogen. Such polypeptide immunogens are reported by Sutcliffe et al., *Nature*, 287:801 (1980), and Lerner et al., *Proc.*  
25 *Natl. Acad. Sci. USA*, 78:3403 (1981).

Gerin et al., *Proc. Natl. Acad. Sci. USA*, 80:2365 (1983), showed limited protection of chimpanzees from hepatitis B virus upon immunization with carrier-bound synthetic polypeptides having  
30 amino acid residue sequences that correspond to the sequence of a determinant portion of HBsAg; in

-3-

particular, residues 110-137 of the "S" (surface) region. However, the carrier protein used in those studies was keyhole limpet hemocyanin (KLH), a T cell-dependent carrier that is not fit for use in medical applications to humans because it is a source of irritation that leads to severe inflammation.

T cell-stimulating carrier proteins capable of enhancing the immunogenicity of haptens that do not produce unacceptable side effects in human subjects are often immunogenic natural proteins. For example, tetanus toxoid (TT) has been frequently used when a carrier suitable for human administration was needed. However, the use of tetanus toxoid as a carrier was restricted due to problems with dosage limitations and risk of sensitization to the toxoid itself. In addition, an epitope-specific suppression of response to the carried hapten can occur in individuals already immunized against tetanus.

The hepatitis B surface protein has been proposed as a carrier for heterologous epitopes. Delpeyroux et al., *Science*, 233:472-475 (1986), reported the use of the HBV surface protein (S protein) as a carrier for a poliovirus polypeptide hapten. Those investigators constructed a recombinant deoxyribonucleic acid (DNA) protein expression vehicle that produces a fusion protein, designated HBsPolioAg, capable of forming particles closely resembling authentic 22-nanometer HBsAg particles. HBsPolioAg consists of HBV S protein having an 11 amino acid residue sequence insert

-4-

corresponding to amino acids 93-103 of capsid protein VPI of poliovirus type 1 (Mahoney strain).

Hepadnavirus nucleocapsid proteins have been used as hapten carriers. Heterologous  
5 immunogenic peptide sequences inserted internally in the hepatitis B core, expressed as fusion particles, elicited very high immune responses in immunized animals in the absence of adjuvants. B.E. Clarke et al. *Vaccines* 91:313-318 (1991); F. Schödel et al. *J.*  
10 *Virol.* 66(1):106-114 (1992). U.S. Patent Nos. 4,818,527, 4,882,145, and 5,143,726, the disclosures of which are incorporated herein by reference, describe the use of the carrier effect with hepatitis B virus nucleocapsid protein to enhance the  
15 immunogenicity of an operatively linked polypeptide hapten. Those patents describe the linking of a polypeptide hapten to hepatitis B virus nucleocapsid protein through an amino acid residue side chain that occurs naturally in the hepatitis B nucleocapsid  
20 protein sequence.

Hepadnavirus nucleocapsid proteins are fairly well studied. SEQ ID NOs:1 and 2 are the DNA and amino acid sequences of the human hepatitis B core protein (HBc), subtype ayw, as described in U.S.  
25 Patent Nos. 4,818,527, 4,882,145, and 5,143,726. Other hepadnavirus nucleocapsid protein sequences are also known in the art, see e.g. SEQ ID NOs: 3-13.

There are reasons to select hepadnavirus nucleocapsid proteins as a carrier over other  
30 carriers used in the art, such as keyhole limpet hemocyanin (KLH), BCG, tetanus toxoid and diphtheria

-5-

toxoid. KLH, BCG, tetanus toxoid and diphtheria  
toxoid are non-particulate, whereas hepadnavirus  
nucleocapsid proteins tend to aggregate into  
"particles". HBc particles tend to have a higher  
5 immunogenicity than hepatitis B surface antigen  
(HBsAg) particles. D.R. Milich et al., *Science*,  
234:1398-1401 (1986). HBc is both a T cell-  
independent and a T cell-dependent immunogen. *Id.*  
HBc is one of the most immunogenic proteins known.  
10 Almost all hepatitis B-infected people develop a  
powerful immune response to core. J.H. Hoofnagle,  
*Semin. Liver Dis.*, 1(1):7-14 (1981). HBc can provide  
universal responsiveness, irrespective of genetic  
background. *Id.* HBc directly activates T cells.  
15 HBc elicits strong  $T_h$  cell responses. HBc is  
efficiently processed and presented by antigen-  
presenting cells. Due to the inherently high  
immunogenicity of HBc, complex adjuvants are  
typically not required, for example, the common and  
20 inexpensive alum is sufficient.

The family *hepadnaviridae* is a family of  
enveloped animal viruses with a core of DNA that  
cause hepatitis B in humans. The *hepadnaviridae* are  
not responsible for human hepatitis A (a single-  
25 stranded RNA enterovirus), human hepatitis C  
(*Flaviridae* family of single stranded RNA virus), or  
human hepatitis D (a closed circular negative-sense  
RNA satellite virus, "delta virus", that requires  
hepatitis B virus for replication). The  
30 *hepadnaviridae* family includes hepatitis viruses of  
other species, e.g. woodchuck, duck, ground squirrel,

-6-

and heron, in addition to human and simian hepatitis B. Hepatitis B (HB) used hereinafter refers to the family *hepadnaviridae*, unless the discussion is referring to a specific example.

5                   Hepatitis B core protein monomers self-assemble into stable aggregates known as hepatitis B core protein particles (HBc particles). For example, human HBc particles are 27 nanometers (nm) in diameter. Conway et al., *Nature*, 386:91-94 (1997),  
10                   describe the structure of human HBc particles at 9 Ångstrom resolution, as determined from cryo-electron micrographs. Bottcher et al., *Nature*, 386:88-91 (1997), describe the polypeptide fold for the human HBc monomers, and provide an approximate numbering  
15                   scheme for the amino acid residues at which alpha helical regions and their linking loop regions form. Bottcher et al. propose a loop from about residues 78 to 82 of the hepatitis B core protein.

                  Using synthetic peptides and monoclonal  
20                   antibodies, the immunodominant loop region of HBc was mapped to about amino acid residues 75 to 83. G. Colucci et al., *J. Immunol.*, 141:4376-4380 (1988). Two immunodominant linear epitopes were reported by other workers at amino acid residues 75 to 85 and 130  
25                   to 140. Salfeld et al. *J. Virol.* 63:798 (1989).

                  Insertion mutants of the hepatitis B core protein still are able to form core particles when foreign epitopes are cloned into the immunodominant loop region of HBc. P. Pumpens et al.,  
30                   *Intervirology*, 38:63-74 (1995). The HBc fusion



-7-

proteins form particles in prokaryotic and eukaryotic expression systems. *Id.*

The ability to use a protein as a carrier for a pendently-linked hapten depends upon several factors that have been studied with respect to HBc. Chemically-reactive amino acid side chains, such as lysine (K), aspartic acid (D), glutamic acid (E), and reduced cysteine residues (C), provide functional groups that can be useful for modifying polypeptides.

The hepatitis B core protein sequence has several chemically-reactive amino acid side chains in the native sequence. Core has three primary amino groups, one at the amino terminus, and two lysine residues (K5 and K96), along with four cysteine residues (C48, C61, C107 and C183). There are several carboxylic acid groups, D (2, 4, 22, 29, 32, 78, 83) and E (8, 14, 40, 43, 46, 64, 77, 113, 117, 145, 179) and the carboxy terminus.

However, the native, unmodified hepatitis B core protein particle does not exhibit appreciable chemical reactivity of the amino acid side chains in the native sequence. The chemical reactivity of an amino acid side chain in a protein depends upon the nature of the amino acid side chain, and its environment in the folded protein.

As is discussed in detail hereinafter, it has now been found that the problem of low reactivity of the amino acid side chains in native hepatitis B nucleocapsid protein can be overcome by inserting a chemically-reactive amino acid side chain into the HBc protein sequence. A strategically modified

-8-

hepadnavirus core protein particle of the present invention exhibits substantially enhanced reactivity toward derivitization of HBc particles with chemically linked haptens, and provides enhanced immunogenicity to those linked hapten.

These modified HBc proteins and their pendently-linked hapten conjugate derivatives are discussed in the disclosure that follows.

#### Brief Summary of the Invention

The present invention relates to a strategically modified hepatitis B core (HBc) protein that is linked to a pendent hapten through chemically-reactive amino acid residue inserted into the HBc sequence. The contemplated strategic modification of HBc is an insert mutation of the HBc protein. A contemplated insert is 1 to about 40 amino acid residues in length, preferably 1 to 10 amino acid residues in length, and includes a chemically-reactive amino acid residue.

The insert is provided to the region corresponding to amino acid residues about 50 to about 100 of the hepatitis B core protein sequence shown in SEQ ID NO:2. The preferred region of insertion corresponds to the hepatitis B core protein immunodominant loop region at about amino acid residue 70 to about 90, more preferably the loop tip region at about amino acid 78 to about 82 and most preferably at amino acid 78 to amino acid 80.

Such an introduced chemically-reactive amino acid residue is characterized in that it has a

-9-

chemically-reactive side chain that provides a chemical group for pendently linking the strategically modified HBc to the hapten. Typically, the chemically-reactive amino acid residue is a  
5 lysine, cysteine, or histidine residue or a carboxyl-containing residue such as aspartic acid or glutamic acid, preferably lysine or a carboxyl-containing residue, and most preferably lysine.

The hapten bonded to the chemically-  
10 reactive amino acid residue is any compound of interest for generating an immune response, and is typically a B cell determinant. Preferably, the hapten is a polypeptide hapten, a carbohydrate hapten, or a non-peptidal/non-saccharidal (chemical)  
15 hapten. In one embodiment of the invention, the hapten is a pathogen-related hapten, such as a B cell determinant of a pathogen.

In another embodiment of a strategically modified hepatitis B core protein conjugate, the  
20 strategically modified hepatitis B core protein also has a T cell stimulating amino acid residue sequence operatively linked to the carboxy terminus of the hepatitis B core amino acid sequence. Preferably, both the hapten and the T cell stimulating amino acid  
25 residue sequence are pathogen-related, most preferably, both are related to (from) the same pathogen.

In the above embodiment of the invention, the response to a B cell epitope is boosted by also  
30 providing the T helper ( $T_h$ ) cell determinant. In this preferred embodiment of the invention, such a  $T_h$  cell

-10-

determinant is from the same pathogen as the B cell determinant hapten that is pendently linked to the strategically modified hepatitis B core protein in order to provide pathogen-specific T cell memory in addition to the hepatitis B core protein antigen-specific T cell memory.

A strategically modified hepatitis B core protein conjugate contains a hapten that is pendently linked to a strategically modified hepatitis B core protein. Looked at differently, a before-described strategically modified hepatitis B core protein can be considered to have three peptide-linked domains, I, II and III (numbered consecutively from the amino terminus). Domain I comprises a sequence that corresponds to residues numbered about 10 to 50 of the amino acid sequence of hepatitis B core protein of SEQ ID NO:2, and preferably corresponds to residues numbered 1 to 50 of that sequence. Domain II is bonded to the carboxy terminal residue of Domain I. Domain II corresponds to residues numbered 50 to 100 of the amino acid sequence of hepatitis B core protein of SEQ ID NO:2. Domain III comprises a sequence that is bonded to the carboxy terminal residue of Domain II. Domain III corresponds to residues numbered 100 to about 140 of the amino acid sequence of hepatitis B core protein, and preferably corresponds to residues numbered 100 to about 149 of that sequence.

In an embodiment of the invention discussed before, a strategically modified hepatitis B core protein additionally has a Domain IV exogenous to HBc

-11-

that is peptide-bonded to the carboxy terminal residue of Domain III to provide a fusion protein. Domain IV is a T cell epitope.

5 A strategically modified hepatitis B core protein particle of the invention is made of assembled heptatitis B core protein where a plurality of the subunits are strategically modified hepatitis B core protein subunits. Also contemplated is a particle comprised of a mixture of strategically  
10 modified hepatitis B core protein subunits and other heptatitis B core protein subunits.

A contemplated strategically modified hepatitis B core protein particle conjugate is comprised of assembled hepatitis B core protein  
15 subunits where a plurality of the subunits are strategically modified hepatitis B core protein subunits. In this embodiment, a hapten is pendently linked to a hepatitis B core protein subunit. Preferably, the hapten is pathogen-related. As  
20 above, a T cell stimulating amino acid residue sequence can be peptide-bonded to the carboxy terminal residue of the sequence corresponding to hepatitis B core protein. Preferably that pathogen-related T cell determinant is related to the same  
25 pathogen as the pathogen-related hapten.

A strategically modified hepatitis B core protein particle conjugate of the invention has pendently-linked hapten. In a contemplated  
embodiment of the particle conjugate, the particle is  
30 made up of a mixture of strategically modified hepatitis B core protein subunits having pendently-

-12-

linked haptens, and other hepatitis B core protein subunits. In one embodiment, about 0.1 to about 0.5 of the strategically modified hepatitis B core protein subunits are pendently linked to a hapten.

5 Also contemplated is a particle conjugate that is made up of a mixture of strategically modified hepatitis B core protein subunits and other hepatitis B core protein subunits.

A before-described strategically modified hepatitis B core protein of the invention includes a peptide insert containing a chemically-reactive amino acid residue. That insert can be, but is typically not itself a separate B cell antigenic determinant, although some B cell immunogenicity of the insert can be exhibited merely because of the placement of the insert into the HBc protein or particle. Such an insert can be and in some embodiments is a T cell epitope. Placement of an insert into the HBc loop region greatly diminishes the HBc immunogenicity and antigenicity of the resulting molecule.

An inoculum of the invention comprises an immunogenic amount of the strategically modified hepatitis B core protein conjugate of the invention. When the pendently-linked hapten is a pathogen-related hapten, the inoculum can be used as a vaccine to protect a mammal treated with the inoculum from that pathogen. Thus, in one embodiment of the invention, a strategically modified hepatitis B core protein conjugate is used as a vaccine to provide protection against the pathogen from which the hapten is derived. More preferably, the inoculum is

-13-

comprised of strategically modified hepatitis B core protein particle conjugate as the immunogen.

The present invention has several benefits and advantages.

5           One benefit of a contemplated modified HBc protein is that the protein can be derivitized while in the aggregated form of HBc particles.

          An advantage of the invention is that the modified HBc protein displays appreciably enhanced  
10       chemical reactivity toward derivitization, as compared to use of the N-terminal primary amine, for example.

          Another benefit of a contemplated modified HBc protein is that the chemistry of derivitization  
15       of such side chains is well-studied, straightforward and relatively predictable.

          Another advantage of a contemplated modified HBc protein is that it enhances the immunologic response to the conjugated hapten with  
20       which it is derivitized.

          Yet another benefit of a contemplated modified HBc protein is that it is unlikely to produce undesirable immunologic side effects in humans.

25           Still further benefits and advantages of the invention will be apparent to the skilled worker from the discussion that follows.

#### Brief Description of the Drawings

30           In the figure forming a portion of this disclosure Scheme 1 illustrates a reaction sequence

-14-

for pendently linking a hapten to a strategically modified hepatitis B core protein (sm-HBc) particle using sulpho-succinimidyl 4-(N-maleimidomethyl) cyclohexane 1-carboxylate (sulpho-SMCC). The sm-HBc particle is depicted as a box having (for purposes of clarity of the figure) a single pendent amino group.

### Detailed Description of the Invention

10

#### A. Definitions

The term "antibody" refers to a molecule that is a member of a family of glycosylated proteins called immunoglobulins, which can specifically combine with an antigen.

15

The word "antigen" has been used historically to designate an entity that is bound by an antibody, and also to designate the entity that induces the production of the antibody. More current usage limits the meaning of antigen to that entity bound by an antibody, whereas the word "immunogen" is used for the entity that induces antibody production. Where an entity discussed herein is both immunogenic and antigenic, reference to it as either an immunogen or antigen will typically be made according to its intended utility.

20

25

The word "hapten" is used to describe molecules that are capable of stimulating an immune response (e.g., production of antibody) when chemically coupled to a protein carrier. The word is often used for small nonantigenic molecules in the

30



-15-

art, but herein, it merely refers to the molecule that is to be pendently linked to the carrier protein, even if it is antigenic or not small.

5 "Antigenic determinant" refers to the actual structural portion of the antigen that is immunologically bound by an antibody combining site or T cell receptor. The term is also used interchangeably with "epitope".

10 The noun "conjugate" as used herein refers to a molecule formed from a hapten pendently linked through an amino acid residue side chain to a carrier.

15 The term "conservative substitution" as used herein denotes that one amino acid residue has been replaced by another, biologically similar residue. Examples of conservative substitutions include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for  
20 another such as between arginine and lysine, between glutamic and aspartic acids or between glutamine and asparagine and the like. The term "conservative substitution" also includes the use of a substituted amino acid in place of an unsubstituted parent amino  
25 acid in place of an unsubstituted parent amino acid provided that antibodies raised to such a polypeptide also immunoreact with the corresponding polypeptide having the unsubstituted amino acid.

30 The term "corresponds" in its various grammatical forms as used in relation to peptide sequences means the peptide sequence described plus

-16-

or minus up to three amino acid residues at either or both of the amino- and carboxy-termini and containing only conservative substitutions in particular amino acid residues along the polypeptide sequence.

5               "Epitope" refers to that portion of a molecule that is specifically bound by a T cell antigen receptor or an antibody combining site. "Epitope" and "determinant" are used interchangeably.

              As used herein, the term "fusion protein" designates at least two amino acid residue sequences not normally found linked together in nature operatively linked together end-to-end (head-to-tail) by a peptide bond between their respective terminal amino acid residues.

15              The phrase "hepatitis B" as used here refers in its broadest context to any member of the family *hepadnaviridae*, a family of enveloped DNA-containing animal viruses that can cause hepatitis B in human.

20              The phrase "HBc" as used here refers to T cell stimulating proteins having an amino acid residue sequence that corresponds to an amino acid residue sequence encoded by the hepatitis B virus (HBV) nucleocapsid protein gene. An exemplary well-known naturally occurring protein encoded by the human HBV nucleocapsid gene is the "core" protein, subtype ayw, having the biological sequences of SEQ ID NOs: 1 and 2. Galibert, et al., *Nature* 281:646 (1979). HBeAg protein, the precursor to HBc, includes the sequence of the hepatitis B core protein and a "pre-core" sequence at the amino terminus

25

30

-17-

thereof, as shown in SEQ ID NOs: 8 and 9 in the case of a ground squirrel hepatitis B nucleocapsid gene. The core protein sequence begins at amino acid position 31 therein, thus corresponding to amino acid residue number 1 of SEQ ID NO:2. The sequences for other hepatitis B core proteins are known in the art. Human hepatitis B virus core protein subtype adr is provided in SEQ ID NOs: 3 and 4, and subtype adw is provided in SEQ ID NOs: 5 and 6. Ono et al., *Nucl. Acids Res.* 11:1747 (1983). Sequences are also provided for woodchuck hepatitis B core protein at SEQ ID NO:7 [Schödel et al., *Adv. Viral Oncol.* 8:73-102 (1989)], ground squirrel at SEQ ID NOs:8 and 9, heron at SEQ ID NOs:10 and 11, and duck at SEQ ID NOs:12 and 13. For clarity, the amino acid numbering system shown in SEQ ID NOs:1 and 2 with respect to human hepatitis B core protein subtype ayw is used as a benchmark herein. Other HBc sequences can be aligned with that sequence using standard biological sequence alignment programs and protocols to determine the amino acid residues that "correspond to the hepatitis B core protein sequence of SEQ ID NO:2", see e.g. Schodel et al., *Adv. Viral Oncol.* 8:73-102 (1989).

If reference is made to a polypeptide portion of any of the above described naturally occurring HBV nucleocapsid gene encoded proteins, that reference is explicit, either by stating, for example, that a T cell stimulating portion of the particular protein is referred to or by explicitly designating the particular portion of the sequence,

-18-

as by indication of the included amino acid residue positions.

The term "immunoreact" in its various forms means specific binding between an antigen as a ligand and a molecule containing an antibody combining site  
5 such as a Fab portion of a whole antibody.

The phrase "operatively linked" as used herein means that the linkage does not interfere with the ability of either of the linked groups to  
10 function as described; e.g., to function as a T or B cell determinant.

The phrase "pendently linked" refers to a single linkage, either direct or via a bridge, from a HBc protein to another molecule at other than the  
15 amino or carboxy termini. The phrase is used herein to describe the linkage between a hapten and a chemically-reactive amino acid side chain of a strategically modified hepatitis B core protein.

"Macromolecular assembly" refers to a non-covalently bonded aggregate of protein subunits.  
20 Typically in this invention, the protein subunit is a strategically modified hepatitis B core protein monomer. As described in more detail hereinafter, those core protein monomers usually self-assemble  
25 into spherical "core particles" having either 90 or 120 core protein dimers (a total of 180 or 240 core protein subunits). A spherical core particle is an example of a macromolecular assembly.

The phrase "pathogen-related" as used  
30 herein designates a B cell or T cell immunogen that is capable of inducing the production of antibodies

-19-

that immunoreact with a pathogen in native form.  
Exemplary pathogen-related B cell and T cell  
immunogens are illustrated hereinafter.

The words "polypeptide" and "peptide" as  
5 used interchangeably throughout the specification and  
designate a linear series of amino acid residues  
connected one to the other by peptide bonds between  
the alpha-amino and carboxy groups of adjacent amino  
acids. Polypeptides can be variety of lengths,  
10 either in their neutral (uncharged) forms or in forms  
which are salts, and either free of modifications  
such as glycosylation, side chain oxidation, or  
phosphorylation or containing these modifications.  
It is well understood in the art that amino acid  
15 residue sequences contain acidic and basic groups,  
and that the particular ionization state exhibited by  
the peptide is dependent on the pH of the surrounding  
medium when the protein is in solution, or that of  
the medium from which it was obtained if the protein  
20 is in solid form. Also included in the definition  
are proteins modified by additional substituents  
attached to the amino acid side chains, such as  
glycosyl units, lipids, or inorganic ions such as  
phosphates, as well as modifications relating to  
25 chemical conversions of the chains, such as oxidation  
of sulfhydryl groups. Thus, "polypeptide" or its  
equivalent terms is intended to include the  
appropriate amino acid residue sequence referenced,  
subject to those of the foregoing modifications which  
30 do not destroy its functionality. A peptide or  
polypeptide used as a hapten typically contains fewer

-20-

than 70 amino acid residues, and more typically contains a linear chain of about 5 to about 40 amino acid residues, and more preferably about 10 to about 25 residues. It is noted that a contemplated polypeptide hapten can be longer than 70 residues, but such a polypeptide is shorter than the naturally occurring protein that shares its sequence.

The word "protein" designates a polypeptide having about 70 or more amino acid residues, and is a naturally occurring entity.

The words "secrete" and "produce" are often used interchangeably in the art as to cells from which antibody molecules are obtained. Cells that produce antibodies may, however, not secrete those molecules into their environment. Herein, the antibody molecules are secreted and are obtained from the blood stream (humoral antibody). Nevertheless, antibodies are generally referred to as being "produced" in keeping with the phrase utilized in the art.

All amino acid residues identified herein are in the natural or L-configuration. In keeping with standard polypeptide nomenclature, [*J. Biol. Chem.*, 243, 3557-59 (1969)], abbreviations for amino acid residues are as shown in the following Table of Correspondence, Table 1.

-21-

Table 1. <u>TABLE OF CORRESPONDENCE</u>		
<u>SYMBOL</u>		
1-Letter	3-Letter	AMINO ACID
Y	Tyr	L-tyrosine
G	Gly	glycine
F	Phe	L-phenylalanine
M	Met	L-methionine
A	Ala	L-alanine
S	Ser	L-serine
I	Ile	L-isoleucine
L	Leu	L-leucine
T	Thr	L-threonine
V	Val	L-valine
P	Pro	L-proline
K	Lys	L-lysine
H	His	L-histidine
Q	Gln	L-glutamine
E	Glu	L-glutamic acid
Z	Glx	L-glutamic acid or L-glutamine
W	Trp	L-tryptophan
R	Arg	L-arginine
D	Asp	L-aspartic acid
N	Asn	L-asparagine
B	Asx	L-aspartic acid or L-asparagine
C	Cys	L-cysteine

## 5 B. Strategically Modified Hepatitis B Core Protein

The present invention contemplates a strategically modified *hepadnaviridae* core ("HBc") protein that has an inserted chemically reactive amino acid residue for pendently linking with haptens

10 such as polypeptides and carbohydrates. The strategic modification of the invention is the

-22-

insertion of 1 to about 40 amino acid residues including a chemically-reactive amino acid residue into the hepatitis B core protein sequence in the region corresponding to amino acid residues 50 to 100 of the HBc sequence of SEQ ID NO:2. Such an introduced chemically-reactive amino acid residue has a side-chain that provides a functional group for pendently linking a hapten to the strategically modified carrier.

10               *Hepadnaviridae* have a nucleocapsid, or core, surrounded by a lipid envelope containing surface proteins. The nucleocapsid is a generally spherical aggregate of core proteins ("core antigen", HBcAg) dimers. In vitro, the hepatitis B core protein self-assembles into "particles", spherical  
15 shells of icosahedral symmetry made up of 90 or 120 hepatitis B core protein dimers, thus 180 or 240 protein subunits. The particles are about 280 or 310 Ångstroms in diameter, respectively. B. Bottcher et al., *Nature*, 386:88-91 (1997); J.F. Conway et al.  
20 *Nature* 386:91-94 (1997).

A contemplated strategically modified hepatitis B core protein also forms a macromolecular assembly. Such a particle can be present in the form  
25 of 180 or 240 protein subunits, although it does not have to be such a 90 or 120 dimer.

Hybrid core proteins with exogenous amino acid residues inserted in the region near amino acid residue 80 are reported to assemble into regular  
30 shells, even with inserts as large as 46 amino acids in length. A.I. Brown et al., *Vaccine*, 9:595-601



-23-

(1991); F. Schödel et al., *J. Virol.*, 66:106-114 (1992).

The *hepadnaviridae* core protein sequence used as a benchmark sequence herein is that of the human hepatitis B core protein, subtype ayw, shown in SEQ ID NOs:1 and 2. Other subtypes of the human hepatitis B virus are known. SEQ ID Nos: 3 and 4 are human HBc, subtype adr, and SEQ ID NOs:5 and 6 are HBc subtype adw. The sequences of various animal hepatitis core proteins are also published. The biological sequence of duck hepatitis core protein is disclosed herein as SEQ ID NO:12 and 13; a portion of the ground squirrel hepatitis nucleocapsid gene is at SEQ ID NO:8 and 9; woodchuck hepatitis core is at SEQ ID NO:7 and heron hepatitis core at SEQ ID NOs:10 and 11. Exemplary animal hepatitis B core proteins are aligned with human hepatitis B core protein by F. Schödel et al., *Adv. Viral Oncology* 8:73-102 (1989).

20 i. Strategic Modification of the Core Protein

The present invention contemplates a strategically modified hepatitis B core protein conjugate that comprises a hapten that is pendently linked to a strategically modified hepatitis B core protein (HBc). The strategically modified hepatitis B core protein itself comprises an amino acid sequence corresponding to the hepatitis B core protein amino acid sequence of SEQ ID NO:2 including the amino acid residues numbered about 10 to about 140 of that sequence. That HBc amino acid residue sequence additionally contains an exogenous amino

-24-

acid residue insert in the region corresponding to amino acid residues numbered about 50 to about 100 from the HBc amino terminus, wherein the exogenous insert (i) is 1 to about 40 amino acid residues in length, and (ii) contains a chemically-reactive amino acid residue. The hapten is pendently linked to the strategically modified HBc protein by means of a chemically-reactive amino acid residue present in the insert.

10                   It is preferred that residues 1 through 10 of SEQ ID NO:2 be present in the strategically modified HBc protein molecule. It is further preferred when any residue is absent or deleted from position 1 to 10 that those residues be deleted in sequence and that the remaining residues be present in sequence. Thus, if a five residue deletion were contemplated, the deleted residues would be numbered 1-5, leaving residues 6 through the desired HBc carboxy terminus present, plus the insert.

20                   It is similarly preferred that residues numbered about position 140 through 149 of SEQ ID NO:2 be present in a strategically modified HBc protein molecule. As noted elsewhere herein, the region of HBc numbered 150 through the carboxy terminus contains a plurality of arginine residues. Those residues bind nucleic acids on purification of HBc particles after expression, and the sequence containing those residues is preferably omitted from a strategically modified HBc protein molecule. As  
25  
30 was the case with the residues of positions 1 through 10, it is preferred that residues between about

-25-

position 140 and 149 be present and correspondingly absent in a sequential manner. Thus, where the carboxy terminal residue corresponds to the residue of position 146, the residues of positions 141-145 are also present and those of 147-149 are absent. Most preferably, a contemplated HBc sequence is that shown in SEQ ID NO:2 from position 1 through position 149, plus the sequence of the insert.

The insert can be placed within the HBc sequence in the region of positions numbered about 50 through about 100, as already noted. Preferably, the insert is present in the region corresponding to amino acid residues numbered about 70 to about 90. More preferably, the insert is present in the region corresponding to amino acid residues numbered 78 to 82. Most preferably, the insert is located in the region corresponding to residues numbered 78 through 80.

A strategically modified hepatitis B core protein of the invention has from 1 to about 40 amino acid residues inserted. Preferably, the insert is 1 to 10 amino acid residues in length. The insert contains a chemically-reactive amino acid residue. The insertion of more than one chemically-reactive amino acid residue is also contemplated.

It is contemplated that restriction endonuclease sites be provided in the gene construct for the strategically modified hepatitis B protein near the desired insert region. The nucleotides of the restriction endonuclease site will be translated into amino acids upon expression, and that effect has

-26-

some bearing on the choice of endonuclease. Several restriction endonucleases are commercially available (e.g. from Promega Corp., Madison, Wisconsin) and their recognition site sequences and cleavage sites well known in the art. Example 1 describes such a construct for a strategically modified hepatitis B core protein.

In one preferred embodiment, the insert is a single residue that is added as the chemically-reactive residue. In other preferred embodiments, the use of restriction enzymes and their recognition sequences causes about three to about five residues to be inserted, including the desired chemically reactive residue.

An insert containing a chemically-reactive amino acid residue is inserted into the native hepatitis B core protein at a position corresponding to an amino acid residue position from about 50 to about 100. The preferred region of insertion into the hepatitis B core protein is in the immunodominant loop region (about amino acid residue 70 to about 90), more preferably in the loop region that corresponds to the native hepatitis B core protein position from about amino acid 78 to about 82. Most preferably, the insert is placed at residues numbered 78 to 80 of SEQ ID NO:2.

As used herein when it is said that the insert is "at a position" it is meant that the amino terminus of the insert is peptide bonded to the carboxy terminus of the corresponding amino acid residue of the hepatitis B core protein sequence

-27-

having that amino acid residue number. In other words, the insert immediately follows the residue at that stated position.

Insertion can be effected by generally  
5 utilized methods in the art. Genetic manipulation, by a PCR-based method is illustrated in Examples 1 and 5. In addition, oligonucleotide-mediated site directed mutagenesis as discussed in J.Sambrook et al. Molecular Cloning: a laboratory manual, 2<sup>nd</sup> ed.,  
10 Cold Spring Harbor Laboratory Press, 15.51-ff. (1989) can be used to add one codon by hybridizing a desired DNA sequence with a template that adds a codon for single residue, followed by filling in the remaining nucleic acid sequence. Dawson et al., Science  
15 266:776-779 (1994), describe a method of linking polypeptide chains at their peptide backbone, so that a fusion could be built up of peptide fragments.

The chemically-reactive amino acid residue can be at any position within the insert.  
20 Preferably, the chemically-reactive amino acid residue is in a position that corresponds to amino acid residue numbered 70 to 90 of the native (wild type) core, and most preferably at residue position 78 to 82. For example, when a 10 amino acid residue  
25 long insert is inserted at a position corresponding to native core protein residue 73, then the chemically-reactive amino acid residue is preferably at position 5 to 9 of the insert. When a 30 amino acid residue long insert is inserted a position  
30 corresponding to native core protein residue 58, then

-28-

the chemically-reactive amino acid residue is preferably at position 22 to 24 of the insert.

An introduced chemically-reactive amino acid residue has a chemically-reactive side chain that provides a functional group for derivitizing the strategically modified HBc (i.e. conjugating a hapten to the modified HBc). Useful side chain functional groups include epsilon-amino groups, beta-or gamma-carboxyl groups, thiol (-SH) groups and aromatic rings (e.g. tyrosine and histidine). The chemically-reactive amino acid residue is typically a lysine, cysteine, or histidine residue or a carboxyl-containing residue such as aspartic acid or glutamic acid. Lysine is a particularly preferred chemically-reactive amino acid residue.

It is noted that the amino acid residue sequence of the hepatitis B core protein encoded by and shown in SEQ ID NOs:1 and 2, respectively, has two consecutive endogenous carboxyl-containing residues, existing glutamic (glu, E) and aspartic (asp, D) acids, at positions 77 and 78. However, the present invention contemplates the introduction of at least one *additional*, exogenous chemically-reactive amino acid residue. European Patent No. 385610 reports that unsatisfactory results were achieved in attempts to chemically couple polypeptide haptens to HBc particles. It is noted that those coupling attempts were directed toward amino groups and not carboxyl groups of the amino acid side chains.

In addition of the use of an individual chemically-reactive amino acid residue in the insert

-29-

such as aspartic acid or lysine, substantially any sequence of the desired length that contains a chemically-reactive amino acid residue can be used. Exemplary inserts of greater than a single residue include the B cell HRV-2 VP2 epitope discussed in B.E. Clarke et al. *Vaccines* 91:313-318 (1991), the HBsAg Pre-S(1)27-53 sequence discussed in F. Schödel et al. *J. Virol.* 66(1):106-114 (1992) and the HBsAg Pre-S(2)133-143 sequence discussed in F. Schödel et al. *Vaccines* 90:193-198 (1990). An appropriate T cell epitope discussed hereinafter as a hapten can also be used as an insert. Exemplary sequences include those of SEQ ID NOS: 28, 32, 33, 34, 47, 48, 49, 50 and 55.

15

ii. Additional Modification of the Core Protein

It is also contemplated that a hepatitis B core protein strategically modified as described above has other modifications. The contemplated modifications of the strategically modified core include the nature of the insert containing the chemically-reactive amino acid residue, truncation of the amino terminus, truncation of the carboxy terminus, fusion at the carboxy terminus, pendent linking to the carboxy-terminal region.

25

The insert containing the chemically-reactive amino acid residue to which the hapten is conjugated can have a use in addition to providing the chemically-reactive amino acid residue. It is contemplated that an insert containing a chemically-reactive amino acid residue is a T cell stimulating

30

-30-

amino acid sequence. Such a T cell stimulating amino acid sequence is preferably a T cell epitope from the same source as the B cell epitope that will be the conjugated antigen, e.g. both from *Mycobacterium*  
5 *tuberculosis*. Exemplary epitopes are discussed hereinafter.

An insert containing a chemically-reactive amino acid residue can also be chosen in order to confer additional desirable properties, such as  
10 stability-enhancing or solubility-enhancing properties.

A strategically modified hepatitis B core protein can be chemically modified by methods well known in the art. Numerous such techniques are  
15 disclosed in Roger L. Lundblad, Techniques in Protein Modification, CRC Press (Ann Arbor, Michigan: 1994). Such chemical modifications are made to enhance or diminish properties, for example, a lysine amino group can be blocked to change the isoelectric point  
20 of the protein, causing it to separate differently on a chromatographic ion exchange resin.

It is also contemplated that the carboxy terminus of the core protein sequence be truncated, preferably down to about amino acid residue position  
25 140. The arginine-rich sequence present beginning at residue 150 of SEQ ID NO:2 binds to nucleic acids and can hinder the purification and handling of the expressed core protein. In SEQ ID NO:2, the arginine-rich stretches begin at position 150. A  
30 preferred strategically modified HBc protein has a carboxy terminal valine (V) residue of residue 149.



iii. Making Strategically-Modified Core Protein

The strategic modification of the hepatitis B core protein is typically made by known processes in the art on the DNA level, for example by inserting the codons corresponding to the amino acids to be inserted. The engineered gene is then expressed in a convenient system known in the art, for example in a viral culture in infected immortalized cells.

Methods for producing HBcAg proteins in general and the pre-core, core and HBeAg proteins in particular, are well known in the art. The same methods readily adapted to the isolation of the modified core protein particles of the invention. In addition, HBcAg and HBeAg can be produced by a variety of well known recombinant DNA techniques. See, for example, U.S. Pat. No. 4,356,270 to Itakura and 4,563,423 to Murray et al., respectively. Those recombinant DNA techniques can be easily adapted to produce modified core particles of the invention. The modified core proteins can be conjugated with hapten before or after particle formation, preferably after core particle formation and purification.

C. Modified Hepatitis B Core Protein Conjugate

Any hapten against which antibody production is desired can be linked to a strategically modified hepatitis B core protein to form an immunogenic strategically modified hepatitis B core protein conjugate of this invention. The hapten of interest typically is a B cell determinant.

-32-

The hapten can be a polypeptide, a carbohydrate (saccharide), or a non-polypeptide, non-carbohydrate chemical such as 2,4-dinitrobenzene.

5       Methods for operatively linking individual  
haptens to a protein or polypeptide through an amino  
acid residue side chain of the protein or polypeptide  
to form a pendently-linked immunogenic conjugate,  
e.g., a branched-chain polypeptide polymer, are well  
known in the art. Those methods include linking  
10       through one or more types of functional groups on  
various side chains and result in the carrier protein  
polypeptide backbone being pendently linked--  
covalently linked (coupled) to the hapten but  
separated by at least one side chain.

15       Methods for linking carrier proteins to  
haptens using each of the above functional groups are  
described in Erlanger, *Method of Enzymology*, 70:85  
(1980), Aurameas, et al., *Scand. J. Immunol.*, Vol. 8,  
Suppl. 7, 7-23 (1978) and U.S. Pat. No. 4,493,795 to  
20       Nestor et al. In addition, a site-directed coupling  
reaction, as described in Rodwell et al., *Biotech.*,  
3, 889-894 (1985) can be carried out so that the  
biological activity of the polypeptides is not  
substantially diminished.

25       Furthermore, as is well known in the art,  
both the HBCAg protein and a polypeptide hapten can  
be used in their native form or their functional  
group content can be modified by succinylation of  
lysine residues or reaction with cysteine-  
30       thiolactone. A sulfhydryl group can also be  
incorporated into either carrier protein or conjugate

-33-

by reaction of amino functions with 2-iminothiolane or the N-hydroxysuccinimide ester of 3-(3-dithiopyridyl)propionate.

The HBc protein or hapten can also be modified to incorporate a spacer arm, such as hexamethylene diamine or other bifunctional molecules of similar size, to facilitate the pendent linking.

*Polypeptide hapten.* Methods for covalent bonding of a polypeptide hapten are extremely varied and are well known by workers skilled in the immunological arts. For example, following U.S. Patent No. 4,818,527, m-maleimidobenzoyl-N-hydroxysuccinimide ester (ICN Biochemicals, Inc.) or succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (SMCC, Pierce) is reacted with a strategically modified hepatitis B core protein to form an activated carrier. That activated carrier is then reacted with a polypeptide that either contains a terminal cysteine or to which an additional amino- or carboxy-terminal cysteine residue has been added to form a covalently bonded strategically modified hepatitis B core protein conjugate. As an alternative example, the amino group of a polypeptide hapten can be first reacted with N-succinimidyl 3-(2-pyridylthio)propionate (SPDP, Pharmacia), and that thiol-containing polypeptide can be reacted with the activated carrier after reduction. Of course, the sulfur-containing moiety and double bond-containing Michael acceptor can be reversed. These reactions are described in the supplier's literature, and also in Kitagawa, et al., *J. Biochem.*, 79:233 (1976) and

in Lachmann et al., in 1986 Synthetic Peptides as Antigens, (Ciba Foundation Symposium 119), pp. 25-40 (Wiley, Chichester: 1986).

U.S. Patent No. 4,767,842 teaches several  
5 modes of covalent attachment between a carrier and polypeptide that are useful here. In one method, tolylene diisocyanate is reacted with the carrier in a dioxane-buffer solvent at zero degrees C to form an activated carrier. A polypeptide hapten is  
10 thereafter admixed and reacted with the activated carrier to form the covalently bonded strategically modified hepatitis B core protein conjugate.

Particularly useful are a large number of heterobifunctional agents that form a disulfide link  
15 at one functional group end and a peptide link at the other, including N-succidimidyl-3-(2-pyridyldithio) propionate (SPDP). This reagent creates a disulfide linkage between itself and a thiol in either the strategically modified hepatitis B core protein or  
20 the hapten, for example a cysteine residue in a polypeptide hapten, and an amide linkage on the coupling partner, for example the amino on a lysine or other free amino group in the carrier protein. A variety of such disulfide/amide forming agents are  
25 known. See for example *Immun. Rev.* (1982) 62:185. Other bifunctional coupling agents form a thioether rather than a disulfide linkage. Many of these thioether-forming agents are commercially available and include reactive esters of 6-maleimidocaproic  
30 acid, 2-bromoacetic acid, 2-iodoacetic acid, 4-(N-maleimido-methyl)cyclohexane-1-carboxylic acid and

the like. The carboxyl groups can be activated by combining them with succinimide or 1-hydroxy-2-nitro-4-sulfonic acid, sodium salt. The particularly preferred coupling agent for the method of this invention is succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC) obtained from Pierce Company, Rockford, Ill. The foregoing list is not meant to be exhaustive, and modifications of the named compounds can clearly be used, e.g., the sulpho-SMCC depicted in the figure.

A polypeptide hapten can be obtained in a number of ways well known in the art. Usual peptide synthesis techniques can be readily utilized. For example, recombinant and PCR-based techniques to produce longer peptides are useful. Because the desired sequences are usually relatively short, solid phase chemical synthesis is useful.

As discussed below, DNA sequences that encode a variety of polypeptide haptens are known in the art. The coding sequence for peptides of the length contemplated herein can easily be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., *J. Am. Chem. Soc.* 103:3185 (1981). Of course, by chemically synthesizing the coding sequence, any desired modification can be made simply by substituting the appropriate bases for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors now commonly available in the art,

-36-

and the regulating vectors used to transform suitable hosts to produce the desired protein.

A number of such vectors and suitable host systems are now available. For example promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. Typical of such vector plasmids are, for example, pUC8, and pUC13 available from J. Messing, at the University of Minnesota (see, e.g., Messing et al., *Nucleic Acids Res.* 9:309 (1981)) or pBR322, available from New England Biolabs. Suitable promoters include, for example, the beta-lactamase (penicillinase) and lactose (lac) promoter systems (Chang. et al., *Nature* 198:1056 (1977) and the tryptophan (trp) promoter system (Goeddel et al., *Nucleic Acids Res.* 8:4057 (1980)). The resulting expression vectors are transformed into suitable bacterial hosts using the calcium chloride method described by Cohen, et al., *Proc. Natl. Acad. Sci. U.S.A.* 69:2110 (1972). Successful transformants may produce the desired polypeptide fragments at higher levels than those found in strains normally producing the intact pili. Of course, yeast or mammalian cell hosts can also be used, employing suitable vectors and control sequences.

Table 2  
Polypeptide haptens

Organism	Antigen	T or B cell epitope	Sequence	SEQ ID NO
<i>Streptococcus pneumoniae</i>	PspA	B	KLEELSDKIDELDAE	25
<i>Streptococcus pneumoniae</i>	PspA	B	SQKKYDEDQKKTEEKAALEKA ASEEMDKAVAAVQQA	26
<i>Cryptosporidium parvum</i>	P23	B	QDKPADAPAAEAPAAEPAAQQ DKPADA	27
HIV	P24	T	GPKEPFRDYVDRFYKC	28
HIV	GP120	B	RKRIHIGPGRIFYITKN	29
Foot and Mouth Disease Virus	VP1	B	YNGECRYNRNAVPNLRGDLQV LAQKVARTLP	30
<i>Corynebacterium diphtheriae</i>	toxin	T	FQVVHNSYNRPAYSPGC	31
<i>Borrelia burgdorferi</i>	OspA	T	VEIKEGTVTLKREIDKNGKVT VSLC	32
<i>Borrelia burgdorferi</i>	OspA	T	TL SKNISKSGEVSVELNDC	33
Influenza A8/PR8	HA	T	SSVSSFERFEC	34
Influenza A8/PR8	HA	B	YRNLLWLTEK	35
<i>Yersinia pestis</i>	V Ag	B	DILKVI VDSMNHG DARS KLR EELAE LTAELKIYSV IQAEIN KHLSSSGTINI HDKSINLMDK NLYGYTDEE I FKASAEYKILE KMPQTTIQVDGSEKKIVSIKD FLGSENKRTGALGNLKNSSYSY NKDNNELSHFATTCS D	36
<i>Haemophilus influenzae</i>	pBOMP	B	CSSSNDAAGNGAAQFGGY	37
<i>Haemophilus influenzae</i>	pBOMP	B	NKLGT VSYGEE	38
<i>Haemophilus influenzae</i>	pBOMP	B	NDEAAYSKNRRAVLAY	39
<i>Moraxella catarrhalis</i>	copB	B	LDIEKDKKKRTDEQLQAE LDD KYAGKGY	40
<i>Moraxella catarrhalis</i>	copB	B	LDIEKNKKKRTEAE LQAE LDD KYAGKGY	41
<i>Moraxella catarrhalis</i>	copB	B	IDIEKKGKIRTEAE LLAELNK DYPGQGY	42

Porphyromonas gingivalis	HA	B	GVSPKVCKDVTVEGSNEFAPV QNLT	43
Porphyromonas gingivalis	HA	B	RIQSTWRQKTVDLPAGTKYV	44
Trypanosoma cruzi		T	SHNFTLVASVIEEAPSGNTC	45
Trypanosoma cruzi		B	KAAIAPAKAAAAPAKAATAPA	46
Plasmodium falciparum	MSP1	T	SVQIPKVPYPNGIVYC	47
Plasmodium falciparum	MSP1	T	DFNHYYTLKTGLEADC	48
Streptococcus sobrinus	AgI/II	B & T	KPRPIYEAKLAQNQKC	49
Streptococcus sobrinus	AgI/II	B & T	AKADYEAKLAQYEKDLG	50
lymphocytic Choriomeningitis virus	NP	T	RPQASGVYMGNLTAQC	51
Shigella flexneri	Invasin	B	KDRTLIEQK	52
respiratory syncytial virus	G	B	CSICSNPTCWAICK	53
Plasmodium vivax	CS	B	GDRADGQPAGDRADGQPAG	54
Clostridium tetani	tox	T	QYIKANSKFIGITELC	55
Entamoeba histolytica	lectin	B	VECASTVCQNDNSCPIIADVE KCNQ	56
Schistosoma japonicum	para	B	DLQSEISLSLENGELIRRAKS AESLASELQRRVD	57
Schistosoma mansoni	para	B	DLQSEISLSLENGELIRRAKA AESLASDLQRRVD	58
Plasmodium vivax		B	DRAAGQPAGDRADGQPAG	83
Influenza virus	Infl	B	CNNPHRIL	84
Influenza virus	Infl	T	CPKYVKQNTLKLATGMRNVPE KQTR	85
Influenza virus	Infl	B	SIMRSDAPIGTCSSSECITPNG SIPNDKPFQNVNKITY	14
Influenza virus	Infl	B	RGIFGAIAGFIENGWEGMIDG WYGFRHQN	15
Influenza virus	Infl	B	EKQTRGIFGA	16
Mycobacterium tuberculosis		T	AVLEDPYILLVSSKV	86
Mycobacterium tuberculosis		T	LLVSSKVSTVKDLLP	87



Mycobacterium tuberculosis		T	LLPLLEKVIGAGKPL	88
Mycobacterium tuberculosis		T	AILTGGQVISEEVGL	89
Mycobacterium tuberculosis		T	IAFNSGLEPGVVAEK	90
Mycobacterium tuberculosis		T	ARRGLERGLNALADAVKV	91
Mycobacterium tuberculosis		T	EKIGAELVKEVAKK	92
Mycobacterium tuberculosis		T	GLKRGIEKAVEKVETL	93
Mycobacterium tuberculosis		T	IEDAVRNAKAAVEEG	94
Feline leukemia virus	FeLV	B	CDIIGNTWNPSDQEPFPGYG	95
Feline leukemia virus	FeLV	B	CIGTVPKTHQALCNETQQGHT	96
Feline leukemia virus	FeLV	B	GNYSNQTNPPPS	97
Feline leukemia virus	FeLV	B	TDIQALEESISALEKSLTSLSE	98
Feline leukemia virus	FeLV		AKLRERLKQRQQLF	99
Feline leukemia virus	FeLV		DSQQGWFEFGWFKSPWFTTLISS	100
Feline leukemia virus	FeLV		QVMTITPPQAMGPNLVLP	101
Feline leukemia virus	FeLV		DQKPPSRQSQIESRVTP	102
Feline leukemia virus	FeLV		RRGLDILFLQEGGLC	103
Feline leukemia virus	FeLV		QEGGLCAALEECQIGGLCAALKEEC	104
Plasmodium falciparum		B	NANPNANPNANP	105
Circumsporozoite			QAQGDGANAGQP	113

*Chemical Hapten.* Related chemistry is used to couple chemical compounds to carrier proteins.

- 5 Typically, an appropriate functional group for coupling is designed into the chemical compound.

Antibodies to the compound 6-O-phosphocholine hydroxyhexanoate protect against *Streptococcus pneumoniae*. Randy T. Fischer et al. *J. Immunol.*, 154:3373-3382 (1995).

10

Table 3  
Chemical Haptens

Chemical Hapten	Citation
piperidine N-oxide	U.S. Patent No. 5,304,252
phospholactone or lactamide	U.S. Patent No. 5,248,611
metal ion complexes	U.S. Patent No. 5,236,825
[2.2.1] or [7.2.2] bicyclic ring compounds	U.S. Patent No. 5,208,152
ionically charged hydroxyl-containing compounds	U.S. Patent No. 5,187,086
phosphonate analogs of carboxylate esters	U.S. Patent No. 5,126,258
cocaine analogs	Carrera et al., <i>Nature</i> 378:725 (1995)

5                    *Carbohydrate Hapten.* There are many methods known in the art to couple carrier proteins to polysaccharides. Aldehyde groups can be generated on either the reducing end [Anderson, *Infect. Immun.*, 39:233-238 (1983); Jennings, et al., *J. Immunol.*, 127:1011-1018 (1981); Poren et al., *Mol. Immunol.*, 22:907-919 (1985)] or the terminal end [Anderson et al., *J. Immunol.*, 137:1181-1186 (1986); Beuvery et al., *Dev. Bio. Scand.*, 65:197-204 (1986)] of an oligosaccharide or relatively small polysaccharide,

10

-41-

which can be linked to the carrier protein via reductive amination.

Large polysaccharides can be conjugated by either terminal activation [Anderson et al., *J. Immunol.*, 137:1181-1186 (1986)] or by random activation of several functional groups along the polysaccharide chain [Chu et al., *Infect. Immun.*, 40:245-256 (1983); Gordon, U.S. Patent 4,619,828 (1986); Marburg, U.S. Patent 4,882,317 (1989)]. Random activation of several functional groups along the polysaccharide chain can lead to a conjugate that is highly cross-linked due to random linkages along the polysaccharide chain. The optimal ratio of polysaccharide to carrier protein depend on the particular polysaccharide, the carrier protein, and the conjugate used.

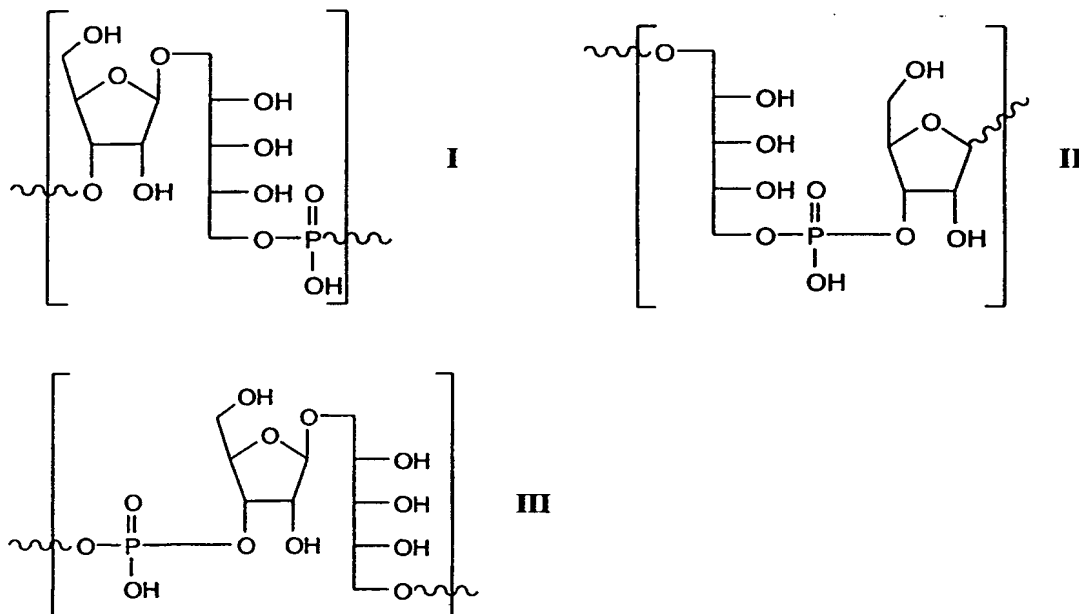
See Dick et al., in Contributions to Microbiology and Immunology, Vol. 10, Cruse et al., eds., (S. Karger: 1989), pp. 48-114; Jennings et al., in Neoglycoconjugates: Preparation and Applications, Lee et al., eds., (Academic Press: 1994), pp. 325-371; Aplin et al., *CRC Crit. Rev. Biochem.*, 10:259-306 (1981); and Stowell et al., *Adv. Carbohydr. Chem. Biochem.*, 37:225-281 (1980) for detailed reviews of methods of conjugation of saccharide to carrier proteins.

The carbohydrate itself can be synthesized by methods known in the art, for example by enzymatic glycoprotein synthesis as described by Witte et al., *J. Am. Chem. Soc.*, 119:2114-2118 (1997).

-42-

Several oligosaccharides, synthetic and semi-synthetic, and natural, are discussed in the following paragraphs as examples of oligosaccharides that are contemplated haptens to be used in making a strategically modified core protein conjugate of the present invention.

An oligosaccharide hapten suitable for preparing vaccines for the treatment of *Haemophilus Influenza* type b (Hib) is made up of from 2 to 20 repeats of D-ribose-D-ribitol-phosphate (I, below), D-ribitol-phosphate-D-ribose (II, below), or phosphate-D-ribose-D-ribitol (III, below). Eduard C. Beuvery et al., EP-0 276 516-B1.



U.S. Patent 4,220,717 also discloses a polyribosyl ribitol phosphate (PRP) hapten for *Haemophilus influenzae* type b.

Ellena M. Peterson et al., *Infection and Immunity*, 66(8):3848-3855 (1998), disclose a trisaccharide hapten,  $\alpha$ Kdo(2 8) $\alpha$ Kdo(2 4) $\alpha$ Kdo, that

-43-

provides protection from *Chlamydia pneumoniae*.

*Chlamydia pneumoniae* is a cause of human respiratory infections ranging from pharyngitis to fatal pneumonia. Kdo is 3-deoxy-D-manno-oct-2-ulosonic acid.

Bengt Andersson et al., EP-0 126 043-A1, disclose saccharides that can be used in the treatment, prophylaxis or diagnosis of bacterial infections caused by *Streptococci pneumoniae*. One class of useful saccharides are derived from the disaccharide GlcNAc $\beta$ 1 3Gal. Andersson et al. also found neolactotetraosylceramide to be useful, which is Gal $\beta$ 1 4GlcNAc $\beta$ 1 3Gal $\beta$ 1 4Glc-Cer.

European Patent No. 0 157 899-B1, the disclosures of which are incorporated herein by reference, discloses the isolation of pneumococcal polysaccharides that are useful in the present invention. The following table lists the pneumococcal culture types that produce capsular polysaccharides useful as haptens in the present invention.

Table 4  
Polysaccharide Hapten Sources

Danish Type Nomenclature	U.S. Nomenclature	1978 ATCC Catalogue Number
1	1	6301
2	2	6302
3	3	6303
4	4	6304
5	5	

-44-

6A	6	6306
6B	26	6326
7F	51	10351
8	8	6308
9N	9	6309
9V	68	
10A	34	
11A	43	
12F	12	6312
14	14	6314
15B	54	
17F	17	
18C	56	10356
19A	57	
19F	19	6319
20	20	6320
22F	22	
23F	23	6323
25	25	6325
33F	70	

*Moraxella (Branhamella) catarrhalis* is a known cause of otitis media and sinusitis in children and lower respiratory tract infections in adults.

- 5 The lipid A portion of the lipooligosaccharide surface antigen (LOS) of the bacterium is cleaved at the 3-deoxy-D-manno-octulosonic acid-glucosamine linkage. The cleavage product is treated with mild-alkali to remove ester-linked fatty acids while
- 10 preserving amide-linked fatty acids to yield

detoxified lipopolysaccharide (dLOS) from *M. catarrhalis*. The dLOS is not immunogenic until it is attached to a protein carrier. Xin-Xing Gu, et al. *Infection and Immunity* 66(5):1891-1897 (1998).

5                   Group B streptococci (GBS) is a cause of sepsis, meningitis, and related neurologic disorders in humans. The Capsular polysaccharide-specific antibodies are known to protect human infants from infection. Jennings et al., U.S. 5,795,580. The  
10                   repeating unit of the GBS capsular polysaccharide type II is: 4)- $\beta$ -D-GlcpNAc-(1 3)-[ $\beta$ -D-Galp(1 6)]- $\beta$ -D-Galp(1 4)- $\beta$ -D-Glcp-(1 3)- $\beta$ -D-Glcp-(1 2)-[ $\alpha$ -D-NeupNAc(2 3)]- $\beta$ -D-Galp-(1 , where the bracketed portion is a branch connected to the immediately  
15                   following unbracketed subunit. The repeating unit of GBS capsular polysaccharide type V is: 4)-[ $\alpha$ -D-NeupNAc-(2 3)- $\beta$ -D-Galp-(1 4)- $\beta$ -D-GlcpNAc-(1 6)]- $\alpha$ -D-Glcp-(1 4)-[ $\beta$ -D-Glcp-(1 3)]- $\beta$ -D-Galp-(1 4)- $\beta$ -D-Glcp-(1 .

20                   European patent application No. EU-0 641 568-A1, Dr. Helmut Brade, discloses the method of obtaining ladder-like banding pattern antigen from *Chlamydia trachomatis*, *pneumoniae* and *psittaci*.

25                   D.   Pathogen-Related Conjugate to the Modified HBc

                  In one embodiment of the invention, the hapten that is conjugated to strategically modified HBc protein is a B cell determinant of a pathogen. B cell determinants of numerous pathogens are known in  
30                   the art, and several were illustrated in the

-46-

preceding discussions of polypeptide and carbohydrate haptens.

In preferred embodiments, the hapten is a pathogen-related hapten. The use of a portion of a pathogen's protein sequence or carbohydrate sequence as a hapten has distinct advantages over the exposure to an actual pathogen, and even over a passivated or "killed" version of the pathogen.

Exemplary pathogen-related haptens of particular importance are derived from bacteria such as *B. pertussis*, *S. typosa*, *S. paratyphoid* A and B, *C. diphtheriae*, *C. tetani*, *C. botulinum*, *C. perfringens*, *B. anthracis*, *P. pestis*, *P. multocida*, *V. cholerae*, *N. meningitides*, *N. gonorrhea*, *H. influenzae*, *T. palladium*, and the like.

Other exemplary sources of pathogen-related haptens of particular importance are viruses such as poliovirus, adenovirus, parainfluenza virus, measles, mumps, respiratory syncytical virus, influenza virus, equine encephalomyelitis virus, hog cholera virus, Newcastle virus, fowl pox virus, rabies virus, feline and canine distemper viruses, foot and mouth disease virus (FMDV), human and simian immunodeficiency viruses, and the like. Other important sources of pathogen-related haptens include rickettsiae, epidemic and endemic typhus, the spotted fever groups, and the like.

Pathogen-related polypeptide haptens are well-known in art and are discussed in numerous disclosures such as U.S. Pat. Nos. 3,149,036, 3,983,228, and 4,069,313; in Essential Immunology, 3<sup>rd</sup>



-47-

Ed., by Roit, published by Blackwell Scientific Publications; in Fundamentals of Clinical Immunology, by Alexander and Good, published by W.B. Saunders; and in Immunology, by Bellanti, published by W.B. Saunders.

5                   Particularly preferred pathogen-related haptens are those described in U.S. Pat. Nos. 4,625,015, 4,544,500, 4,545,931, 4,663,436, 4,631,191, 4,629,783 and in Patent Cooperation Treaty  
10                  International Publication No. WO87/02775 and No. WO87/02892, all of whose disclosures are incorporated herein by reference.

                  Antibodies that immunoreact with the hepatitis B virus can be obtained by using modified  
15                  HBc conjugated with a polypeptide hapten that corresponds to the sequence of a determinant portion of HBsAg; in particular, residues 110-137 of the "S" (surface) region disclosed in Gerin et al., *Proc. Natl. Acad. Sci. USA*, 80:2365 (1983).

20                  Another conjugate corresponds to amino acids 93-103 of capsid protein VPI of poliovirus type 1 (PV1, Mahoney strain), analogous to the work by Delpeyroux et al., *Science*, 233:472-475 (1986). Such a modified HBc conjugate provides antibodies that  
25                  immunoreact with polio. Other potential haptens from poliovirus type 1, Mahoney and Sabin strains are described in European Patent No. 385610.

                  In preferred embodiments, the hapten is a pathogen-related hapten that immunoreacts with; i.e.,  
30                  is immunologically bound by, antibodies induced by the pathogen. More preferably, the pathogen-related

-48-

hapten induces an antibody response that provides protection against infection by the pathogen.

Methods for determining the presence of antibodies to an immunogen in a body sample from an immunized animal are well known in the art. Methods for determining the presence of both cross-reactive and protective antibodies are well known in the art.

In another embodiment of the invention, the immune response to the B cell determinant is boosted by also providing a T cell determinant.

For example, U.S. Patent No. 4,882,145 describes T cell stimulating polypeptides derived from the HBV nucleocapsid protein. Other T cell determinants are known in the art and can be used as an operatively linked determinant in a contemplated modified HBc protein or particle.

In a particularly preferred embodiment of the invention, such a T cell determinant is derived from the same pathogen as the B cell determinant that is conjugated to the modified HBc. The T cell determinants of various pathogens are reported in the art.

Although it is preferred that the B and T cell determinants are derived from the same pathogen, it is not necessary that they be from the same protein of that pathogen. For example, the B cell determinant from the VP1 protein of the foot and mouth disease virus (FMDV) can be conjugated to a modified HBc particle, wherein the HBc protein is further modified by having a T cell determinant derived from the VP4 protein of FMDV.

-49-

The additional T cell determinant can be introduced into a modified HBc protein on the genetic level using well-known methods within or at a terminus of the HBc protein sequence (amino or  
5 carboxy termini), including as part of the DNA inserted to introduce the chemically-reactive amino acid residue, but preferably as a fusion protein at the carboxy terminus. Alternatively, the additional  
10 T cell determinant can be operatively linked to the conjugated B cell determinant or the strategically modified HBc protein.

Exemplary disclosures that describe techniques for genetically engineering a DNA sequence that can be used to produce a fusion protein of the  
15 present invention can be found in: U.S. Pat. Nos. 4,428,941 to Galibert et al., 4,237,224 to Cohen et al.: 4,273,875 to Manis; 4,431,739 to Riggs; 4,363,877 to Goodman et al., and Rodriguez & Tait, *Recombinant DNA Techniques: An Introduction*, The  
20 Benjamin-Cummings Publishing Co., Inc. Menlo Park, Calif. (1983), whose disclosures are incorporated by reference.

#### E. Inocula and Vaccines

25 In yet another embodiment of the invention, a modified HBc protein or particle conjugated to a hapten (a HBc conjugate) is used as the immunogen of an inoculum that induces production of antibodies that immunoreact with the hapten or as a vaccine to  
30 provide protection against the pathogen from which the hapten is derived.

-50-

A contemplated inoculum or vaccine comprises a HBcAg conjugate that is dissolved or dispersed in a pharmaceutically acceptable diluent composition that typically also contains water. When administered in an immunogenic effective amount to an animal such as a mammal (e.g., a mouse, dog, goat, sheep, horse, bovine, monkey, ape, or human) or bird (e.g., a chicken, turkey, duck or goose), an inoculum induces antibodies that immunoreact with the conjugated (pendently-linked) hapten. A vaccine is a type of inoculum in which the hapten is pathogen related and the induced antibodies not only immunoreact with the hapten, but also immunoreact with the pathogen or diseased cell, and neutralize the pathogen or diseased cell with which they immunoreact.

The preparation of inocula and vaccines that contain proteinaceous materials as active ingredients is also well understood in the art. Typically, such inocula or vaccines are prepared as parenterals, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The immunogenic active ingredient is often mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, an inoculum or vaccine can contain minor amounts of auxiliary

-51-

substances such as wetting or emulsifying agents, pH buffering agents or adjuvants which enhance the immunogenic effectiveness of the composition.

Exemplary adjuvants include complete  
5 Freund's adjuvant (CFA) that is not used in humans, incomplete Freund's adjuvant (IFA) and alum, which are materials well known in the art, and are available commercially from several sources. The use of small molecule adjuvants is also contemplated  
10 herein.

Exemplary of one group of small molecule adjuvants are the so-called muramyl dipeptide analogues described in U.S. Patent No. 4,767,842. Another type of small molecule adjuvant described in  
15 U.S. Patent No. 4,787,482 that is also useful herein is a 4:1 by volume mixture of squalene or squalane and Aracel™ A (mannide monooleate).

Yet another type of small molecule adjuvant useful herein is a 7-substituted-8-oxo or 8-sulfo-  
20 guanosine derivative described in U.S. Patents No. 4,539,205, No. 4,643,992, No. 5,011,828 and No. 5,093,318, whose disclosures are incorporated by reference. Of these materials, 7-allyl-8-oxoguanosine (loxoribine) is particularly preferred.  
25 That molecule has been shown to be particularly effective in inducing an antigen-(immunogen-)specific response

Inocula and vaccines are conventionally administered parenterally, by injection, for example,  
30 either subcutaneously or intramuscularly. Additional formulations that are suitable for other modes of

administration include suppositories and, in some cases, oral formulation or by nasal spray. For suppositories, traditional binders and carriers can include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like.

An inoculum or vaccine composition takes the form of a solution, suspension, tablet, pill, capsule, sustained release formulation or powder, and contains an immunogenic amount of strategically modified HBc protein conjugate or strategically modified HBc protein particle conjugate as active ingredient. In a typical composition, an immunogenic amount of strategically modified HBc protein conjugate or strategically modified HBc protein particle conjugate is about 50  $\mu$ g to about 2 mg of active ingredient per dose, and more preferably about 100  $\mu$ g to about 1 mg per dose.

The particles and protein conjugates can be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic,

-53-

oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The inocula or vaccines are administered in a manner compatible with the dosage formulation, and in such amount as are therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, capacity of the subject's immune system to synthesize antibodies, and degree of protection desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. However, suitable dosage ranges are of the order of several hundred micrograms active ingredient per individual. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed in intervals (weeks or months) by a subsequent injection or other administration.

Another embodiment of the invention is a process for inducing antibodies in an animal host comprising the steps of inoculating said animal host with an inoculum. The inoculum used in the process comprises an immunogenic amount of a strategically modified hepatitis B core protein conjugate dissolved or dispersed in a pharmaceutically acceptable

-54-

diluent. The strategically modified hepatitis B core protein conjugate used in the process comprises a hapten pendently linked to a strategically modified hepatitis B core protein. Preferably the

5 strategically modified hepatitis B core protein is in particle form. The strategically modified hepatitis B core protein comprises an amino acid sequence corresponding to the hepatitis B core protein amino acid sequence of SEQ ID NO:2 including the amino acid

10 residues numbered about 10 to about 140 and additionally having an insert in the region corresponding to amino acid residues numbered about 50 to about 100, said insert (i) being 1 to about 40 amino acid residues in length, and (ii) containing a

15 chemically-reactive amino acid residue. The hapten is pendently linked to the strategically modified hepatitis B core protein through said chemically-reactive amino acid residue. Preferably, the hapten is pathogen-related. The animal is maintained for a

20 time sufficient for antibodies to be induced.

The invention is illustrated by the following non-limiting examples.

25 Example 1: Construction of a Modified Hepatitis B  
Core Protein Expression Vector

Using site-directed mutagenesis, a lysine codon (TTT) was introduced between amino acids D78 and P79 of the HBc gene, along with EcoRI (GAATTC)

30 and SacI (GAGCTC) restriction endonuclease sites to facilitate the genetic insertion of other condons for



-55-

producing strategically modified hybrid HBc particles. The insert thus had an amino acid residue sequence GIQKEL, where the GIQ is an artifact of the EcoRI site and the EL is an artifact of the SacI site. The strategically modified hepatitis B core protein was therefore 155 amino acid residues long. The construction of the pKK322-HBc155-K81 expression plasmid is described below.

Oligonucleotide primers P1F (SEQ ID NO:17) and P1R (SEQ ID NO:18, on the complementary strand) were used to amplify the 5' end of the HBc gene (bases 1-234, amino acids 1-78), and simultaneously incorporate an NcoI restriction site (CCATGG) at the 5' end, and an EcoRI restriction site (GAATTC) at the 3' end of the amplified product. Oligonucleotide primers (SEQ ID NO:19) P2F and P2R (SEQ ID NO:20, on the complementary strand) were used to amplify the 3' end of the HBc gene (bases 232-450, amino acids 79-149), and simultaneously incorporate an EcoRI restriction site (GAATTC) at the 5' end, a SacI restriction site (GAGCTC) adjacent to it, an inserted lysine codon (AAA) between them, and a HindIII restriction site at (AAGCTT) the 3' end of the amplified product.

The two PCR products (encoding amino acids 1-78 and amino acids 79-149) were cleaved with EcoRI, ligated together at their common EcoRI overhangs, cleaved with NcoI and HindIII and cloned into the expression plasmid pKK332 (Pharmacia), using standard techniques. The resulting plasmid was called pKK332-HBc-K81. This plasmid can be used for the expression

-56-

of a strategically modified HBc protein bearing a lysine in the immunodominant loop. The expressed strategically modified HBc protein spontaneously formed particles. The strategically modified HBc of this Example thus had an insert corresponding to position 78 of the HBc of SEQ ID NO:2, a chemically reactive lysine residue at a position corresponding to position 82 of the HBc of SEQ ID NO:2, and was truncated at a position corresponding to position 149 of the HBc of SEQ ID NO:2.

-57-

## Example 2: Modified Hepatitis B Core

Particle Purification

Strategically modified HBc particles of Example 1 were expressed in E. coli typically E. coli BLR or BL21 from Novagen (Madison, Wisconsin) or E. coli TB11 from Amersham (Arlington Heights, Illinois). The transfected E. coli denoted HBc155-K81, were expressed plasmid pKK332-HBc155-K81. The strategically modified HBc particles were purified via Sepharose CL-4B chromatography using established procedures. Because particles purify in a predictable manner, the monitoring of particle elution using simple spectroscopy ( $OD_{280}$ ), in concert with SDS-PAGE analysis to assess purity of individual fractions prior to pooling, was sufficient to enable the routine purification of electrophoretically pure particles in high yield (5-120 mg/L cell culture). The spherical structure of the pure strategically modified hepatitis B core particles was clearly visible in an electron micrograph.

Example 3: Chemical Coupling of Synthetic  
Peptides and Modified Hepatitis  
B Core Particles

The strategically modified hepatitis B core particle product of the expression plasmid pKK332-HBc155-K81 from Example 1 was assayed for its chemical reactivity compared with similarly expressed and purified "wild type" truncated hepatitis B core particle HBc149, which is identical to HBc155-K81

-58-

except that it lacks the introduced lysine residue and flanking five amino acids.

Synthetic peptides (haptens) were chemically conjugated to HBC particles using  
5 succinimidyl 4-(N-maleimido-methyl) cyclohexane  
1-carboxylate (SMCC), a water-soluble  
heterobifunctional cross-linking reagent. SMCC is  
reactive towards both sulfhydryl and primary amino  
groups, enabling the sequential conjugation of  
10 synthetic peptides to HBC particles whose primary  
amino groups have previously been modified with SMCC.  
Further, the 11.6 angstrom spacer arm afforded by  
SMCC helps to reduce steric hindrance between the  
hapten and the HBC carrier, thereby enabling higher  
15 coupling efficiencies.

Briefly, HBC155-K81 and HBC149 particles  
were separately reacted with a 3-fold excess of SMCC  
over total amino groups (native amino groups or  
native amino groups plus the one from the lysine  
20 residue of the insert) for 2 hours at room  
temperature in 50 mM sodium phosphate, pH 7.5, to  
form maleimide-activated HBC particles. Unreacted  
SMCC was removed by repeated dialysis against 50 mM  
sodium phosphate, pH 7.0. The SMCC derivitization of  
25 the HBC particles resulted in a minimal molecular  
weight increase which was not detectable by SDS-PAGE.  
However, the PAGE analysis did confirm the integrity  
of the HBC proteins prior to proceeding to the  
peptide conjugation step.

30 Synthetic peptides to be coupled to the HBC  
particles were designed such that they had N-terminal

-59-

cysteine residues to enable directional conjugation of peptide haptens to the primary amine on the side chain of the introduced lysine residue via the cysteine sulfhydryl of the hapten.

- 5                   Table 2 shows the synthetic peptides derived from human cytochrome P450 enzymes that were chemically conjugated to HBc particles. The synthetic peptides were dissolved in 50 mM sodium phosphate, pH 7.0, to a concentration of 10 mg/ml.
- 10   The synthetic peptides were then added, dropwise, to a 5-fold excess over total amino groups in maleimide-activated strategically modified HBc155-K81 particles, and permitted to react at room temperature for 2 hours. Maleimide-activated HBc149 particles
- 15   were reacted with the two 2D6 peptides (206 and 206-C) as controls.

-60-

Table 5  
Cytochrome P-450 Haptens

	Peptide Name	Sequence	SEQ ID NO.:
5	1A1 (289-302)	CQEKQLDENANVQL	21
	1A2 (291-302)	CSKKGPRASGNLI	22
	2D6 (263-277)	CLTEHRMTWDPAQPPRDLT	23
	3A4 (253-273)	CVKRMKESRLEDTQKHRVDFLQ	24
	1A1-c	CMQLRS	106
10	1A2-c	CRFSIN	107
	2D6-c	CAVPR	108
	2E1-c	CIPRS	109
	2C-c	CFIPV	110
	3A3/4/7-c	CTVSGA	111
15	3A5-c	CTLSGE	112

Example 4: Analysis of Modified Core  
Particles Conjugates

20 Strategically modified HBc particles  
pendently linked to cytochrome P-450 determinant  
haptens of Example 3 were analyzed by SDS-PAGE and  
immunoblots to determine if synthetic peptides had  
been successfully conjugated to HBc. The denaturing  
25 conditions of the electrophoresis disassemble of  
particles into their constituent subunits, HBc  
monomers. Because HBc monomers have a molecular  
weight of approximately 16,000 Da, it was simple to  
resolve HBc155-K81 particles chemically conjugated to  
30 either 1A1 (289-302), 1A2 (291-302), 2D6 (263-277) or  
3A4 (253-273) peptides, as those peptides have a

-61-

relative molecular mass of approximately 2,000 Da and therefore cause a visible increase in the molecular mass of the HBc protein monomers. From the relative intensities of the conjugated and non-conjugated bands on SDS-PAGE, it was revealed that approximately 50 percent of the HBc155-K81 monomers were operatively linked to hapten, whereas only about 5 percent of the "wild type" HBc149 particles were linked to hapten. The marked increase in the observed success in pendently linking hapten to the strategically modified hepatitis B core protein supports the conclusion that the observed linking occurs via the inserted lysine as opposed to a lysine residue that is also present in the "wild type".

The shift in mobility of HBc particles conjugated to shorter C-terminal P450 derived peptides (5 and 6-mers) is not as pronounced in the SDS-PAGE as that of the longer inhibitory peptides, but shifts of approximately 700 Da were clearly evident in successfully coupled HBc155-K81 monomers. The strategically modified HBc 155-K81 protein exhibited markedly enhanced ability to pendently link to a hapten over the "wild type" HBc149 particles, which showed minimal conjugation.

In the model of core particles propounded by Conway et al. of icosahedral particles of either 180 or 240 associated core protein monomers [Nature, 386:91-94 (1997)], dimers of the relatively exposed immunodominant loop regions of the core monomers extend out from the assembled core particle into solution like spikes on a mace. The "spikes" are

-62-

closely arranged spatially on the HBc particles. The strategic location of the introduced lysine residue on the tip of the spike minimizes the propensity for steric constraints to reactions to link haptens to the assembled core particle. A maximum of 50 percent of the strategically modified HBc monomers were successfully conjugated to the synthetic peptides of Cyt P-450. That amount of pendent linkage corresponds to an average of one hapten attached per core particle spike. This proposed distribution of hapten linkage to the strategically modified HBc particle is supported by PAGE results under semi-denaturing conditions that disassemble the particle while maintaining the dimer association.

HBc-2D6 particles, prepared by peptide coupling, were examined using immunoblots to confirm the presentation of the 2D6 epitope. When probed with anti-HBc antisera, the chemically coupled particle yielded two different monomers representing particles with and without the 2D6 peptide. Only the upper band of which blotted with anti-2D6 antisera, thereby confirming the correlation between mobility shift and attachment of the 2D6 peptide.

Example 6: Strategic Lysine Insertions

To construct HBc particles with inserted lysine residues at every position in the immunodominant, surface-exposed loop region (amino acids 75-85), PCR was used to amplify the 5' and 3' fragments of the HBc gene and a single lysine codon was introduced via the oligonucleotide primers. The



-63-

oligonucleotide primers and the resulting amino acid sequences are shown in SEQ ID NOs: 61-82. The "wild type" sequences are SEQ ID NOs:59-60.

In order to generate lysine inserts at positions 75 to 84 (HBc-K75 through HBc-K84), the pairs of PCR fragments were digested with the restriction endonuclease *MseI*, which recognizes the sequence, AATT. The modified gene was restored by ligating the oligonucleotide primer (containing the lysine) at the convenient *MseI* restriction site located at nucleotides 221-224. For HBc-K85 (SEQ ID NOs:85-86) it was necessary to generate two fragments that were ligated at a common *XhoI* restriction site (CTCGAG) that is not present in the wild type gene, but could be introduced at position 239-244 without altering any amino acids.

Table 6

Lysine insertion mutants of HBc  
in the immunodominant loop

Name	Sequence	SEQ ID NO:
Wild Type HBc	TWVGVNLEDPASRD LVVS YV	60
K75	TWVG V <u>K</u> NLEDPASRD LVVS YV	62
K76	TWVG V N <u>K</u> LEDPASRD LVVS YV	64
K77	TWVG V N L <u>K</u> EDPASRD LVVS YV	66
K78	TWVG V N L E <u>K</u> DPASRD LVVS YV	68
K79	TWVG V N L E D <u>K</u> PASRD LVVS YV	70
K80	TWVG V N L E D P <u>K</u> ASRD LVVS YV	72
K81	TWVG V N L E D P A <u>K</u> SRD LVVS YV	74
K82	TWVG V N L E D P A S <u>K</u> RD LVVS YV	76

- 64 -

K83	TWVGVNLEDPASR <u>K</u> DLVVS <del>Y</del> V	78
K84	TWVGVNLEDPASRD <u>K</u> LVVS <del>Y</del> V	80
K85	TWVGVNLEDPASRDL <u>K</u> VVS <del>Y</del> V	82

To purify the strategically modified HBc proteins, cleared cell lysates from a 1L fermentation were precipitated with 45% ammonium sulfate and the resultant pellet subjected to gel filtration using Sepharose CL-4B chromatography (2.5cm x 100cm). Particulate HBc has a characteristic elution position when analyzed using this type of column, which was independent of the amino acid insertions made to the particle. The eleven strategically modified HBc particles generated for this study were analyzed using this procedure, and the elution profiles were measured spectrophotometrically at an absorbance of 280 nm.

Three of the constructs (HBc-K75, HBc-K77, and HBc-K79) were produced at levels of between 50 and 100 mg/L, which is comparable with typical yields for wild-type, unmodified HBc particles, e.g. HBc149 particles. Four of the constructs (HBc-K76, HBc-K78, HBc-K81, and HBc-K82) were produced at relatively low levels of between 1 and 20 mg/L. Finally, four of the particles (HBc-K80, HBc-K83, HBc-K84, and HBc-K85) were produced at levels deemed to be barely detectable (< 1 mg/L).

-65-

Table 7

Yields of purified lysine-containing  
HBc particles from a 1L fermentation

Particle	Yield(mg/L)
HBc-150(K75)	77
HBc-150(K76)	5
HBc-150(K77)	74
HBc-150(K78)	10
HBc-150(K79)	94
HBc-150(K80)	0
HBc-150(K81)	17
HBc-150(K82)	1
HBc-150(K83)	0
HBc-150(K84)	0
HBc-150(K85)	0

5

The foregoing description of the invention,  
including the specific embodiments and examples, is  
intended to be illustrative of the present invention  
and is not to be taken as limiting. Numerous other  
variations and modifications can be effected without  
departing from the true spirit and scope of the  
present invention.

10

-66-

What is claimed:

1. A strategically modified hepatitis B core protein conjugate comprising a strategically modified hepadnavirus nucleocapsid protein pendently linked to a hapten, wherein the strategically modified hepatitis B core protein comprises an amino acid sequence corresponding to the hepatitis B core protein amino acid sequence of SEQ ID NO:2 including the amino acid residues numbered about 10 to about 140 and additionally having an insert in the region corresponding to amino acid residues numbered about 50 to about 100, said insert (i) being 1 to about 40 amino acid residues in length, and (ii) containing a chemically-reactive amino acid residue, said hapten being pendently linked to said chemically-reactive amino acid residue.

2. The strategically modified hepatitis B core protein conjugate according to claim 1 wherein the insert is in the region corresponding to amino acid residues numbered about 70 to about 90.

3. The strategically modified hepatitis B core protein conjugate according to claim 1 wherein the insert is in the region corresponding to amino acid residues numbered 78 to 82.

4. The strategically modified hepatitis B core protein conjugate according to claim 1 wherein

-67-

the hapten is a polypeptide hapten, chemical hapten or carbohydrate hapten.

5           5.    The strategically modified hepatitis B core protein conjugate according to claim 1 wherein the hapten is a pathogen-related hapten.

10           6.    The strategically modified hepatitis B core protein conjugate according to claim 5 wherein the strategically modified hepatitis B core protein further comprises a T cell stimulating amino acid residue sequence operatively linked to the carboxy terminus of said hepatitis B amino acid sequence.

15           7.    The strategically modified hepatitis B core protein conjugate according to claim 6 wherein said T cell stimulating amino acid residue sequence is related to the same pathogen as the pendently linked pathogen-related hapten.

20           8.    A strategically modified hepatitis B core protein particle comprising a strategically modified hepatitis B core protein subunit having an insert containing a chemically-reactive amino acid side chain, said insert not itself an antigenic determinant.

30           9.    A strategically modified hepatitis B core protein particle conjugate comprising a plurality of strategically modified hepatitis B core protein subunits pendently linked to a hapten.

-68-

10. The strategically modified hepatitis B core protein particle conjugate according to claim 9 wherein about 0.1 to about 0.5 of the strategically modified hepatitis B core protein subunits are pendently linked to a hapten.

11. The strategically modified hepatitis B core protein particle conjugate according to claim 9 having a plurality of strategically modified hepatitis B core protein subunits that are pendently linked to different haptens.

12. The strategically modified hepatitis B core protein particle conjugate according to claim 9 wherein the strategically modified hepatitis B core protein subunit further comprises a T cell stimulating amino acid residue sequence peptide-bonded to the carboxy terminal residue of the amino acid sequence corresponding to said hepatitis B amino acid sequence.

13. The strategically modified hepatitis B core protein particle conjugate according to claim 12 wherein the T cell stimulating amino acid residue is from the same pathogen as the pendently linked hapten.

14. An immunogenic fusion protein conjugate comprising a polypeptide hapten pendently linked to a strategically modified hepatitis B core

-69-

protein that comprises three peptide-linked domains,  
I, II and III from the N-terminus, wherein

(a) Domain I corresponds to residues about  
10 through 50 of the amino acid sequence of hepatitis  
5 B core protein of SEQ ID NO:2;

(b) Domain II is bonded to the carboxy  
terminal residue of Domain I and corresponds to  
residues 50 to 100 of said amino acid sequence of  
hepatitis B core protein that further contains a  
10 heterologous insert 1 to about 40 amino acid residues  
in length that includes a chemically-reactive amino  
acid residue; and

(c) Domain III is bonded to the carboxy  
terminal residue of Domain II and corresponds to  
15 residues 100 to about 140 of the amino acid sequence  
of hepatitis B core protein.

15. An immunogenic fusion protein  
conjugate according to claim 14 wherein the  
20 strategically modified hepatitis B core protein  
further comprises a fourth peptide-linked domain,  
Domain IV, wherein

(d) Domain IV is bonded to the carboxy  
terminal residue of Domain III and comprises a T cell  
25 epitope.

16. A strategically-modified hepatitis B  
core protein comprising an amino acid sequence  
corresponding to about amino acid residue 10 to about  
30 amino acid residue 140 of the hepatitis B amino acid  
sequence of SEQ ID NO:2 and having an amino acid

-70-

sequence insert in the region corresponding to about  
residue 50 to about residue 100 of the hepatitis B,  
wherein the insert includes a chemically-reactive  
amino acid residue and the insert itself is not an  
5 antigenic determinant.

17. An inoculum comprising an immunogenic  
amount of a strategically modified hepatitis B core  
protein conjugate dissolved or dispersed in a  
10 pharmaceutically acceptable diluent, said  
strategically modified hepatitis B core protein  
conjugate comprising a hapten pendently linked to a  
strategically modified hepatitis B core protein,  
wherein the strategically modified hepatitis B core  
15 protein comprises an amino acid sequence  
corresponding to the hepatitis B core protein amino  
acid sequence of SEQ ID NO:2 including the amino acid  
residues numbered about 10 to about 140 and  
additionally having an insert in the region  
20 corresponding to amino acid residues numbered about  
50 to about 100, said insert (i) being 1 to about 40  
amino acid residues in length, and (ii) containing a  
chemically-reactive amino acid residue, said hapten  
being pendently linked to said chemically-reactive  
25 amino acid residue.

18. The inoculum according to claim 17  
wherein said strategically modified hepatitis B core  
protein conjugate is present in the form of  
30 particles.



-71-

19. The inoculum according to claim 18 wherein said hapten is from a pathogen and wherein use of said inoculum in a mammalian host protects said mammalian host from said pathogen.

5

20. A process for inducing antibodies in an animal host comprising the steps of inoculating said animal host with an inoculum that comprises an immunogenic amount of a strategically modified hepatitis B core protein conjugate dissolved or  
10 dispersed in a pharmaceutically acceptable diluent, said strategically modified hepatitis B core protein conjugate comprising a hapten pendently linked to a strategically modified hepatitis B core protein,  
15 wherein the strategically modified hepatitis B core protein comprises an amino acid sequence corresponding to the hepatitis B core protein amino acid sequence of SEQ ID NO:2 including the amino acid residues numbered about 10 to about 140 and  
20 additionally having an insert in the region corresponding to amino acid residues numbered about 50 to about 100, said insert (i) being 1 to about 40 amino acid residues in length, and (ii) containing a chemically-reactive amino acid residue, said hapten  
25 being pendently linked to said strategically modified hepatitis B core protein through said chemically-reactive amino acid residue, and maintaining said animal for a time sufficient for antibodies to be induced.

30

-72-

21. The process according to claim 20 wherein said strategically modified hepatitis B core protein conjugate is present in the form of particles.

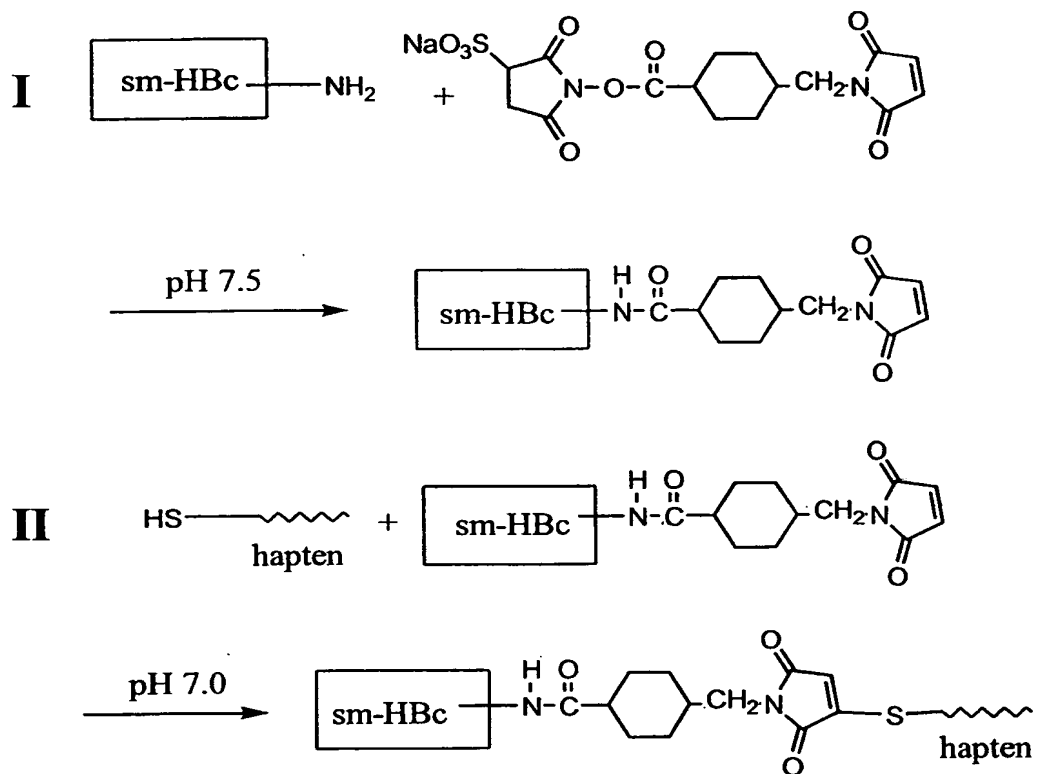
5

22. process according to claim 21 wherein said hapten is from a pathogen and wherein the antibodies induced in said mammalian host protect said mammalian host from said pathogen.

10

1/1

### Scheme 1



## SEQUENCE LISTING

<110> Birkett, Ashley J.  
Immune Complex Inc.

<120> Strategically Modified Hepatitis B Core Proteins and  
their Derivatives

<130> SYN-101 4564/69529

<140> PCT/US99/

<141> 1999-02-11

<150> 60/074537

<151> 1998-02-12

<160> 113

<170> PatentIn Ver. 2.0

<210> 1

<211> 553

<212> DNA

<213> Hepatitis B virus

<220>

<221> CDS

<222> (1) .. (549)

<300>

<303> Nature

<304> 281

<306> 646-

<307> 1979

<400> 1

atg	gac	atc	gac	cct	tat	aaa	gaa	ttt	gga	gct	act	gtg	gag	tta	ctc	48
Met	Asp	Ile	Asp	Pro	Tyr	Lys	Glu	Phe	Gly	Ala	Thr	Val	Glu	Leu	Leu	
1				5					10					15		

tcg	ttt	ttg	cct	tct	gac	ttc	ttt	cct	tca	gta	cga	gat	ctt	cta	gat	96
Ser	Phe	Leu	Pro	Ser	Asp	Phe	Phe	Pro	Ser	Val	Arg	Asp	Leu	Leu	Asp	
			20					25					30			

acc	gcc	tca	gct	ctg	tat	cgg	gaa	gcc	tta	gag	tct	cct	gag	cat	tgt	144
Thr	Ala	Ser	Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys	
			35					40					45			

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg ggg gaa 192  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60

cta atg act cta gct acc tgg gtg ggt gtt aat ttg gaa gat cca gcg 240  
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
 65 70 75 80

tct aga gac cta gta gtc agt tat gtc aac act aat atg ggc cta aag 288  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
 85 90 95

ttc agg caa ctc ttg tgg ttt cac att tct tgt ctc act ttt gga aga 336  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110

gaa aca gtt ata gag tat ttg gtg tct ttc gga gtg tgg att cgc act 384  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125

cct cca gct tat aga cca cca aat gcc cct atc cta tca aca ctt ccg 432  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140

gag act act gtt gtt aga cga cga ggc agg tcc cct aga aga aga act 480  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160

ccc tcg cct cgc aga cga agg tct caa tcg ccg cgt cgc aga aga tct 528  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175

caa tct cgg gaa tct caa tgt tagt 553  
 Gln Ser Arg Glu Ser Gln Cys  
 180

&lt;210&gt; 2

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Hepatitis B virus

&lt;400&gt; 2

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
           35                          40                          45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
           50                          55                          60  
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala  
           65                          70                          75                          80  
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys  
                           85                          90                          95  
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
                           100                          105                          110  
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
           115                          120                          125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
           130                          135                          140  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
           145                          150                          155                          160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
                           165                          170                          175  
 Gln Ser Arg Glu Ser Gln Cys  
           180

<210> 3  
 <211> 552  
 <212> DNA  
 <213> Hepatitis B virus

<220>  
 <221> CDS  
 <222> (1) .. (549)

<300>  
 <303> Nucleic Acids Res.  
 <304> 11  
 <306> 1747-  
 <307> 1983

<400> 3  
 atg gac att gac ccg tat aaa gaa ttt gga gca tct gtg gag tta ctc 48

Met	Asp	Ile	Asp	Pro	Tyr	Lys	Glu	Phe	Gly	Ala	Ser	Val	Glu	Leu	Leu	
1				5					10					15		
tct	ttt	ttg	cct	tct	gac	ttc	ttt	ccg	tct	att	cga	gat	ctc	ctt	gac	96
Ser	Phe	Leu	Pro	Ser	Asp	Phe	Phe	Pro	Ser	Ile	Arg	Asp	Leu	Leu	Asp	
			20					25					30			
acc	gcc	tct	gct	ctg	tat	cgg	gag	gcc	tta	gag	tct	ccg	gaa	cat	tgt	144
Thr	Ala	Ser	Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys	
			35				40					45				
tca	cct	cac	cat	aca	gca	ctc	agg	caa	gct	att	ctg	tgt	tgg	ggg	gag	192
Ser	Pro	His	His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Glu	
	50						55				60					
tta	atg	aat	ctg	gcc	acc	tgg	gtg	gga	agt	aat	ttg	gaa	gac	cca	gca	240
Leu	Met	Asn	Leu	Ala	Thr	Trp	Val	Gly	Ser	Asn	Leu	Glu	Asp	Pro	Ala	
65					70				75					80		
tcc	agg	gaa	tta	gta	gtc	agc	tat	gtc	aat	ggt	aat	atg	ggc	cta	aaa	288
Ser	Arg	Glu	Leu	Val	Val	Ser	Tyr	Val	Asn	Val	Asn	Met	Gly	Leu	Lys	
				85					90					95		
atc	aga	caa	cta	ttg	tgg	ttt	cac	att	tcc	tgc	ctt	act	ttt	gga	aga	336
Ile	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Cys	Leu	Thr	Phe	Gly	Arg	
			100					105					110			
gaa	act	gtt	ttg	gag	tat	ttg	gta	tct	ttt	gga	gtg	tgg	att	cgc	act	384
Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp	Ile	Arg	Thr	
		115					120					125				
cct	ccc	gct	tac	aga	cca	cca	aat	gcc	cct	atc	tta	tca	aca	ctt	ccg	432
Pro	Pro	Ala	Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser	Thr	Leu	Pro	
		130					135					140				
gaa	act	act	gtt	gtt	aga	cga	cga	ggc	agg	tcc	cct	aga	aga	aga	act	480
Glu	Thr	Thr	Val	Val	Arg	Arg	Arg	Gly	Arg	Ser	Pro	Arg	Arg	Arg	Thr	
145					150				155					160		
ccc	tcg	cct	cgc	aga	cga	agg	tct	caa	tcg	ccg	cgt	cgc	aga	aga	tct	528
Pro	Ser	Pro	Arg	Arg	Arg	Arg	Ser	Gln	Ser	Pro	Arg	Arg	Arg	Arg	Ser	
				165				170					175			
caa	tct	cgg	gaa	tct	caa	tgt	tag									552
Gln	Ser	Arg	Glu	Ser	Gln	Cys										
				180												

<210> 4  
 <211> 183  
 <212> PRT  
 <213> Hepatitis B virus

<400> 4  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Val Glu Leu Leu  
 1 5 10 15  
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp  
 20 25 30  
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
 35 40 45  
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
 50 55 60  
 Leu Met Asn Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala  
 65 70 75 80  
 Ser Arg Glu Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys  
 85 90 95  
 Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
 100 105 110  
 Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
 115 120 125  
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
 130 135 140  
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr  
 145 150 155 160  
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser  
 165 170 175  
 Gln Ser Arg Glu Ser Gln Cys  
 180

<210> 5  
 <211> 558  
 <212> DNA  
 <213> Hepatitis B virus



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (555)

&lt;300&gt;

&lt;303&gt; Nucleic Acids Res.

&lt;304&gt; 11

&lt;306&gt; 1747-

&lt;307&gt; 1983

&lt;400&gt; 5

atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc	48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu	
1 5 10 15	

tcg ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctc cta gac	96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp	
20 25 30	

acc gcc tca gct ctg tat cga gaa gcc tta gag tct cct gag cat tgc	144
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys	
35 40 45	

tca cct cac cat act gca ctc agg caa gcc att ctc tgc tgg ggg gaa	192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu	
50 55 60	

ttg atg act cta gct acc tgg gtg ggt aat aat ttg caa gat cca gca	240
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Gln Asp Pro Ala	
65 70 75 80	

tcc aga gat cta gta gtc aat tat gtt aat act aac atg ggt tta aag	288
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys	
85 90 95	

atc agg caa cta ttg tgg ttt cat ata tct tgc ctt act ttt gga aga	336
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg	
100 105 110	

gag act gta ctt gaa tat ttg gtc tct ttc gga gtg tgg att cgc act	384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr	
115 120 125	

cct cca gcc tat aga cca cca aat gcc cct atc tta tca aca ctt ccg	432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro	
130 135 140	

gaa act act gtt gtt aga cga cgg gac cga ggc agg tcc cct aga aga	480
---	-----

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg  
145 150 155 160

aga act ccc tcg cct cgc aga cgc aga tct caa tcg ccg cgt cgc aga 528  
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
165 170 175

aga tct caa tct cgg gaa tct caa tgt tag 558  
Arg Ser Gln Ser Arg Glu Ser Gln Cys  
180 185

<210> 6

<211> 185

<212> PRT

<213> Hepatitis B virus

<400> 6

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu  
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp  
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys  
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu  
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Gln Asp Pro Ala  
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys  
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg  
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg  
145 150 155 160

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
                                   165                                  170                                  175

Arg Ser Gln Ser Arg Glu Ser Gln Cys  
                                   180                                  185

<210> 7  
 <211> 188  
 <212> PRT  
 <213> Hepatitis B virus

<300>  
 <301> Schodel, Florian  
       et al.,  
 <302> Animal Hepatitis B Viruses  
 <303> Adv. Viral Oncol.  
 <304> 8  
 <306> 73-102  
 <307> 1989

<400> 7  
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu  
   1                                  5                                  10                                  15

Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp  
                                   20                                  25                                  30

Thr Ala Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys  
                                   35                                  40                                  45

Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu  
                                   50                                  55                                  60

Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln  
   65                                  70                                  75                                  80

Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys  
                                   85                                  90                                  95

Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln  
                                   100                                  105                                  110

His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr  
                                   115                                  120                                  125

Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro  
                                   130                                  135                                  140

Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser  
 145 150 155 160

Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro  
 165 170 175

Arg Arg Arg Arg Ser Gln Ser Pro Ser Ala Asn Cys  
 180 185

<210> 8  
 <211> 654  
 <212> DNA  
 <213> Hepatitis B virus

<220>  
 <221> CDS  
 <222> (1)..(651)

<300>  
 <302> Animal Hepatitis B Viruses  
 <303> Adv. Viral Oncol.  
 <304> 8  
 <306> 73-102  
 <307> 1989

<400> 8  
 atg tat ctt ttt cac ctg tgc ctt gtt ttt gcc tgt gtt cca tgt cct 48  
 Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro  
 1 5 10 15

act gtt caa gcc tcc aag ctg tgc ctt gga tgg ctt tgg gac atg gac 96  
 Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp  
 20 25 30

ata gat ccc tat aaa gaa ttt ggt tct tct tat cag ttg ttg aat ttt 144  
 Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe  
 35 40 45

ctt cct ttg gac ttt ttt cct gat ctc aat gca ttg gtg gac act gct 192  
 Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala  
 50 55 60

gct gct ctt tat gaa gaa gaa tta aca ggt agg gag cat tgt tct cct 240  
 Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro  
 65 70 75 80

cat cat act gct att aga cag gcc tta gtg tgt tgg gaa gaa tta act 288  
 His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr  
                     85                                    90                                    95

aga tta att aca tgg atg agt gaa aat aca aca gaa gaa gtt aga aga 336  
 Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg  
                     100                                    105                                    110

att att gtt gat cat gtc aat aat act tgg gga ctt aaa gta aga cag 384  
 Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln  
                     115                                    120                                    125

act tta tgg ttt cat tta tca tgt ctt act ttt gga caa cac aca gtt 432  
 Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val  
                     130                                    135                                    140

caa gaa ttt ttg gtt agt ttt gga gta tgg att aga act cca gct cct 480  
 Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro  
                     145                                    150                                    155                                    160

tat aga cca cct aat gca ccc att tta tca act ctt ccg gaa cat aca 528  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr  
                     165                                    170                                    175

gtc att agg aga aga gga ggt tca aga gct gct agg tcc ccc cga aga 576  
 Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg  
                     180                                    185                                    190

cgc act ccc tct cct cgc agg aga agg tct caa tca ccg cgt cgc aga 624  
 Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
                     195                                    200                                    205

cgc tct caa tct cca gct tcc aac tgc tga 654  
 Arg Ser Gln Ser Pro Ala Ser Asn Cys  
                     210                                    215

<210> 9

<211> 217

<212> PRT

<213> Hepatitis B virus

<400> 9

Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro  
                     1                                    5                                    10                                    15

Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp  
                     20                                    25                                    30

Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe  
           35                          40                          45  
 Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala  
           50                          55                          60  
 Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro  
           65                          70                          75                          80  
 His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr  
                           85                          90                          95  
 Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg  
                          100                         105                         110  
 Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln  
           115                         120                         125  
 Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val  
           130                         135                         140  
 Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro  
           145                         150                         155                         160  
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr  
                          165                         170                         175  
 Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg  
                          180                         185                         190  
 Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg  
           195                         200                         205  
 Arg Ser Gln Ser Pro Ala Ser Asn Cys  
           210                         215

<210> 10  
 <211> 918  
 <212> DNA  
 <213> Hepatitis B virus

<220>  
 <221> CDS  
 <222> (1)..(915)

<400> 10

atg tgg tct cta aga tta cac ccc tct cca ttc gga gct gcg tgc caa	48
Met Trp Ser Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln	
1 5 10 15	
ggt atc ttt acg tcg acc tcg ctg ttg ttc ctt gtg act gta cct ttg	96
Gly Ile Phe Thr Ser Thr Ser Leu Leu Phe Leu Val Thr Val Pro Leu	
20 25 30	
gta tgt acc att gtt tat gat tct tgc tta tat atg gat gtc aat gct	144
Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Tyr Met Asp Val Asn Ala	
35 40 45	
tca aga gct tta gca aat gta tat gat ctg cca gat gat ttc ttt cct	192
Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro	
50 55 60	
cag att gat gat ctt gtt aga gat gct aag gat gct tta gaa cct tat	240
Gln Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr	
65 70 75 80	
tgg aaa gcc gaa aca ata aag aaa cat gtt tta att gct act cac ttt	288
Trp Lys Ala Glu Thr Ile Lys Lys His Val Leu Ile Ala Thr His Phe	
85 90 95	
gtg gat ttg att gag gac ttc tgg cag acc act cag ggt atg agc caa	336
Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met Ser Gln	
100 105 110	
att gca gac gcc ctc cga gca gta att cca cct act acc gta cca gta	384
Ile Ala Asp Ala Leu Arg Ala Val Ile Pro Pro Thr Thr Val Pro Val	
115 120 125	
ccg gag ggt ttt ctc att act cat agt gag gca gaa gag atc ccc ttg	432
Pro Glu Gly Phe Leu Ile Thr His Ser Glu Ala Glu Glu Ile Pro Leu	
130 135 140	
aac gat ctc ttt tca aat caa gag gag agg ata gtc aat ttc caa cct	480
Asn Asp Leu Phe Ser Asn Gln Glu Glu Arg Ile Val Asn Phe Gln Pro	
145 150 155 160	
gac tat ccc att aca gct aga att cat acc cac tta cgt gtt tat act	528
Asp Tyr Pro Ile Thr Ala Arg Ile His Thr His Leu Arg Val Tyr Thr	
165 170 175	
aaa ttg aat gaa caa gct ttg gac aaa gct cgc aga ttg ctt tgg tgg	576
Lys Leu Asn Glu Gln Ala Leu Asp Lys Ala Arg Arg Leu Leu Trp Trp	
180 185 190	

cat tac aat tgc ctc ctc tgg gga gaa gcc act gtt aca aat tat att 624  
 His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr Val Thr Asn Tyr Ile  
 195 200 205

tct cgc ctc cgt act tgg ctt tct act ccc gaa aaa tat cga ggc aag 672  
 Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys  
 210 215 220

gat gcc cca acc att gaa gca atc act aga cca atc cag gtg gct caa 720  
 Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln  
 225 230 235 240

gga ggc aga aat caa act aag gga act aga aaa cct cgt gga ctc gaa 768  
 Gly Gly Arg Asn Gln Thr Lys Gly Thr Arg Lys Pro Arg Gly Leu Glu  
 245 250 255

cct aga aga cga aag gtt aaa acc aca gtt gtc tat ggg aga aga cgt 816  
 Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val Tyr Gly Arg Arg Arg  
 260 265 270

tct aag tcc cga ggc agg aga tcc tct cca tcc caa cgt gcg ggc tcc 864  
 Ser Lys Ser Arg Gly Arg Arg Ser Ser Pro Ser Gln Arg Ala Gly Ser  
 275 280 285

cct ctc cca cgt aat cgg gga aac cag aca cga tcc ccc tca cct agg 912  
 Pro Leu Pro Arg Asn Arg Gly Asn Gln Thr Arg Ser Pro Ser Pro Arg  
 290 295 300

gaa tag 918  
 Glu  
 305

<210> 11  
 <211> 305  
 <212> PRT  
 <213> Hepatitis B virus

<400> 11  
 Met Trp Ser Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln  
 1 5 10 15

Gly Ile Phe Thr Ser Thr Ser Leu Leu Phe Leu Val Thr Val Pro Leu  
 20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Tyr Met Asp Val Asn Ala  
 35 40 45



Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro  
 50 55 60

Gln Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr  
 65 70 75 80

Trp Lys Ala Glu Thr Ile Lys Lys His Val Leu Ile Ala Thr His Phe  
 85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met Ser Gln  
 100 105 110

Ile Ala Asp Ala Leu Arg Ala Val Ile Pro Pro Thr Thr Val Pro Val  
 115 120 125

Pro Glu Gly Phe Leu Ile Thr His Ser Glu Ala Glu Glu Ile Pro Leu  
 130 135 140

Asn Asp Leu Phe Ser Asn Gln Glu Glu Arg Ile Val Asn Phe Gln Pro  
 145 150 155 160

Asp Tyr Pro Ile Thr Ala Arg Ile His Thr His Leu Arg Val Tyr Thr  
 165 170 175

Lys Leu Asn Glu Gln Ala Leu Asp Lys Ala Arg Arg Leu Leu Trp Trp  
 180 185 190

His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr Val Thr Asn Tyr Ile  
 195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys  
 210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln  
 225 230 235 240

Gly Gly Arg Asn Gln Thr Lys Gly Thr Arg Lys Pro Arg Gly Leu Glu  
 245 250 255

Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val Tyr Gly Arg Arg Arg  
 260 265 270

Ser Lys Ser Arg Gly Arg Arg Ser Ser Pro Ser Gln Arg Ala Gly Ser  
 275 280 285

Pro Leu Pro Arg Asn Arg Gly Asn Gln Thr Arg Ser Pro Ser Pro Arg  
 290 295 300

Glu  
305

<210> 12

<211> 918

<212> DNA

<213> Hepatitis B virus

<220>

<221> CDS

<222> (1) .. (915)

<400> 12

atg	tgg	aac	tta	aga	att	aca	ccc	ctc	tcc	ttc	gga	gct	gct	tgc	caa	48
Met	Trp	Asn	Leu	Arg	Ile	Thr	Pro	Leu	Ser	Phe	Gly	Ala	Ala	Cys	Gln	
1				5					10					15		

ggt	atc	ttt	acg	tct	aca	ttg	ctg	ttg	tcg	tgt	gtg	act	gta	cct	ttg	96
Gly	Ile	Phe	Thr	Ser	Thr	Leu	Leu	Leu	Ser	Cys	Val	Thr	Val	Pro	Leu	
			20					25					30			

gta	tgt	acc	att	gtt	tat	gat	tct	tgc	tta	tat	atg	gat	atc	aat	gct	144
Val	Cys	Thr	Ile	Val	Tyr	Asp	Ser	Cys	Leu	Tyr	Met	Asp	Ile	Asn	Ala	
		35					40					45				

tct	aga	gcc	tta	gcc	aat	gtg	tat	gat	cta	cca	gat	gat	ttc	ttt	cca	192
Ser	Arg	Ala	Leu	Ala	Asn	Val	Tyr	Asp	Leu	Pro	Asp	Asp	Phe	Phe	Pro	
	50					55					60					

aaa	ata	gat	gat	ctt	gtt	aga	gat	gct	aaa	gac	gct	tta	gag	cct	tat	240
Lys	Ile	Asp	Asp	Leu	Val	Arg	Asp	Ala	Lys	Asp	Ala	Leu	Glu	Pro	Tyr	
65					70				75					80		

tgg	aaa	tca	gat	tca	ata	aag	aaa	cat	gtt	ttg	att	gca	act	cac	ttt	288
Trp	Lys	Ser	Asp	Ser	Ile	Lys	Lys	His	Val	Leu	Ile	Ala	Thr	His	Phe	
				85					90					95		

gtg	gat	ctc	att	gaa	gac	ttc	tgg	cag	act	aca	cag	ggc	atg	cat	gaa	336
Val	Asp	Leu	Ile	Glu	Asp	Phe	Trp	Gln	Thr	Thr	Gln	Gly	Met	His	Glu	
		100						105					110			

ata	gcc	gaa	tca	tta	aga	gct	gtt	ata	cct	ccc	act	act	act	cct	gtt	384
Ile	Ala	Glu	Ser	Leu	Arg	Ala	Val	Ile	Pro	Pro	Thr	Thr	Pro	Pro	Val	
		115					120					125				

cca	ccg	ggt	tat	ctt	att	cag	cac	gag	gaa	gct	gaa	gag	ata	cct	ttg	432
Pro	Pro	Gly	Tyr	Leu	Ile	Gln	His	Glu	Glu	Ala	Glu	Glu	Ile	Pro	Leu	

130	135	140	
gga gat tta ttt aaa cac caa gaa gaa agg ata gta agt ttc caa ccc			480
Gly Asp Leu Phe Lys His Gln Glu Glu Arg Ile Val Ser Phe Gln Pro			
145	150	155	160
gac tat ccg att acg gct aga att cat gct cat ttg aaa gct tat gca			528
Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala			
	165	170	175
aaa att aac gag gaa tca ctg gat agg gct agg aga ttg ctt tgg tgg			576
Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp			
	180	185	190
cat tac aac tgt tta ctg tgg gga gaa gct caa gtt act aac tat att			624
His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Gln Val Thr Asn Tyr Ile			
	195	200	205
tct cgt ttg cgt act tgg ttg tca act cct gag aaa tat aga ggt aga			672
Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Arg			
	210	215	220
gat gcc ccg acc att gaa gca atc act aga cca atc cag gtg gct cag			720
Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln			
	225	230	235
gga ggc aga aaa aca act acg ggt act aga aaa cct cgt gga ctc gaa			768
Gly Gly Arg Lys Thr Thr Thr Gly Thr Arg Lys Pro Arg Gly Leu Glu			
	245	250	255
cct aga aga aga aaa gtt aaa acc aca gtt gtc tat ggg aga aga cgt			816
Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val Tyr Gly Arg Arg Arg			
	260	265	270
tca aag tcc cgg gaa agg aga gcc cct aca ccc caa cgt gcg ggc tcc			864
Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser			
	275	280	285
cct ctc cca cgt agt tcg agc agc cac cat aga tct ccc tcg cct agg			912
Pro Leu Pro Arg Ser Ser Ser Ser His His Arg Ser Pro Ser Pro Arg			
	290	295	300
aaa taa			918
Lys			
305			

&lt;210&gt; 13

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Hepatitis B virus

&lt;400&gt; 13

Met Trp Asn Leu Arg Ile Thr Pro Leu Ser Phe Gly Ala Ala Cys Gln  
 1 5 10 15

Gly Ile Phe Thr Ser Thr Leu Leu Leu Ser Cys Val Thr Val Pro Leu  
 20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Tyr Met Asp Ile Asn Ala  
 35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro  
 50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr  
 65 70 75 80

Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe  
 85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu  
 100 105 110

Ile Ala Glu Ser Leu Arg Ala Val Ile Pro Pro Thr Thr Thr Pro Val  
 115 120 125

Pro Pro Gly Tyr Leu Ile Gln His Glu Glu Ala Glu Glu Ile Pro Leu  
 130 135 140

Gly Asp Leu Phe Lys His Gln Glu Glu Arg Ile Val Ser Phe Gln Pro  
 145 150 155 160

Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala  
 165 170 175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp  
 180 185 190

His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Gln Val Thr Asn Tyr Ile  
 195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Arg  
 210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln

225                      230                      235                      240  
 Gly Gly Arg Lys Thr Thr Thr Gly Thr Arg Lys Pro Arg Gly Leu Glu  
                          245                      250                      255  
 Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val Tyr Gly Arg Arg Arg  
                          260                      265                      270  
 Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser  
                          275                      280                      285  
 Pro Leu Pro Arg Ser Ser Ser Ser His His Arg Ser Pro Ser Pro Arg  
                          290                      295                      300

Lys  
 305

<210> 14  
 <211> 37  
 <212> PRT  
 <213> Influenza virus

<400> 14  
 Ser Ile Met Arg Ser Asp Ala Pro Ile Gly Thr Cys Ser Ser Glu Cys  
   1                          5                          10                          15  
 Ile Thr Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val  
                           20                          25                          30  
 Asn Lys Ile Thr Tyr  
                           35

<210> 15  
 <211> 29  
 <212> PRT  
 <213> Influenza virus

<400> 15  
 Arg Gly Ile Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu  
   1                          5                          10                          15  
 Gly Met Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn  
                           20                          25

<210> 16

<211> 10  
<212> PRT  
<213> Influenza virus

<400> 16  
Glu Lys Gln Thr Arg Gly Ile Phe Gly Ala  
1 5 10

<210> 17  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hepatitis B  
virus PCR primer with an NcoI restriction site

<400> 17  
ttgggccatg gacatcgacc tta 23

<210> 18  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hepatitis B  
virus PCR primer with an EcoRI restriction site

<400> 18  
gcggaattcc atcttccaaa ttaacaccca c 31

<210> 19  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hepatitis B  
virus PCR primer with EcoRI and SacI restriction  
sites and an inserted lysine codon

<400> 19  
cgcggaattca aaaagagctc ccagcgtcta gagagaccta g 41

<210> 20  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hepatitis B  
virus PCR primer with HindIII restriction site

<400> 20  
cgcaagctta aacaacagta gtctccgga g 31

<210> 21  
<211> 14  
<212> PRT  
<213> Hepatitis B virus

<400> 21  
Cys Gln Glu Lys Gln Leu Asp Glu Asn Ala Asn Val Gln Leu  
1 5 10

<210> 22  
<211> 13  
<212> PRT  
<213> Hepatitis B virus

<400> 22  
Cys Ser Lys Lys Gly Pro Arg Ala Ser Gly Asn Leu Ile  
1 5 10

<210> 23  
<211> 19  
<212> PRT  
<213> Hepatitis B virus

<400> 23  
Cys Leu Thr Glu His Arg Met Thr Trp Asp Pro Ala Gln Pro Pro Arg  
1 5 10 15

Asp Leu Thr

<210> 24

<211> 22  
<212> PRT  
<213> Hepatitis B virus

<400> 24  
Cys Val Lys Arg Met Lys Glu Ser Arg Leu Glu Asp Thr Gln Lys His  
1 5 10 15

Arg Val Asp Phe Leu Gln  
20

<210> 25  
<211> 15  
<212> PRT  
<213> Streptococcus pneumoniae

<300>  
<310> EP-0 786 521-A

<400> 25  
Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu  
1 5 10 15

<210> 26  
<211> 35  
<212> PRT  
<213> Streptococcus pneumoniae

<300>  
<310> EP-0 786 521-A

<400> 26  
Gln Lys Lys Tyr Asp Glu Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala  
1 5 10 15

Leu Glu Lys Ala Ala Ser Glu Glu Met Asp Lys Ala Val Ala Ala Val  
20 25 30

Gln Gln Ala  
35

<210> 27  
<211> 31  
<212> PRT  
<213> Cryptosporidium parvum



&lt;300&gt;

&lt;310&gt; WO 98/07320

&lt;400&gt; 27

Gln Asp Lys Pro Ala Asp Ala Pro Ala Ala Glu Ala Pro Ala Ala Glu  
1 5 10 15

Pro Ala Ala Glu Pro Ala Ala Gln Gln Asp Lys Pro Ala Asp Ala  
20 25 30

&lt;210&gt; 28

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Human immunodeficiency virus

&lt;300&gt;

&lt;310&gt; US 5,639,854

&lt;400&gt; 28

Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Cys  
1 5 10 15

&lt;210&gt; 29

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Human immunodeficiency virus

&lt;300&gt;

&lt;310&gt; WO 98/07320

&lt;400&gt; 29

Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ile Thr Lys  
1 5 10 15

Asn

&lt;210&gt; 30

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Foot-and-mouth disease virus

&lt;300&gt;

&lt;310&gt; US 4,544,500

&lt;400&gt; 30

Tyr Asn Gly Glu Cys Arg Tyr Asn Arg Asn Ala Val Pro Asn Leu Arg  
1 5 10 15

Gly Asp Leu Gln Val Leu Ala Gln Lys Val Ala Arg Thr Leu Pro  
20 25 30

&lt;210&gt; 31

&lt;211&gt; 17

&lt;212&gt; PRT

<213> *Corynebacterium diphtheriae*

&lt;300&gt;

&lt;310&gt; EP-0 399 011-B1

&lt;400&gt; 31

Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly  
1 5 10 15

Cys

&lt;210&gt; 32

&lt;211&gt; 25

&lt;212&gt; PRT

<213> *Borrelia burgdorferi*

&lt;300&gt;

<301> Bockenstedt, L. K.  
et al.,

&lt;303&gt; J. Immunol.

&lt;304&gt; 157

&lt;305&gt; 12

&lt;306&gt; 5496-

&lt;307&gt; (1966)

&lt;400&gt; 32

Val Glu Ile Lys Glu Gly Thr Val Thr Leu Lys Arg Glu Ile Asp Lys  
1 5 10 15

Asn Gly Lys Val Thr Val Ser Leu Cys  
20 25

&lt;210&gt; 33

<211> 19  
<212> PRT  
<213> *Borrelia burgdorferi*

<300>  
<301> Zhong, W.  
et al.,  
<303> Eur. J. Immunol.  
<304> 26  
<305> 11  
<306> 2749-  
<307> 1996

<400> 33  
Thr Leu Ser Lys Asn Ile Ser Lys Ser Gly Glu Val Ser Val Glu Leu  
1 5 10 15

Asn Asp Cys

<210> 34  
<211> 11  
<212> PRT  
<213> Influenza A virus

<300>  
<301> Brumeanu, T. D.  
<303> Immunotechnology  
<304> 2  
<305> 2  
<306> 85-  
<307> (1996)

<400> 34  
Ser Ser Val Ser Ser Phe Glu Arg Phe Glu Cys  
1 5 10

<210> 35  
<211> 10  
<212> PRT  
<213> Influenza A virus

<300>  
<301> Brumeanu, T. D.  
<303> Immunotechnology  
<304> 2

<305> 2  
<306> 85-  
<307> (1996)

<400> 35  
Tyr Arg Asn Leu Leu Trp Leu Thr Glu Lys  
1 5 10

<210> 36  
<211> 142  
<212> PRT  
<213> *Yersinia pestis*

<300>  
<301> Hill, J.  
et al.,  
<303> Infect. Immun.  
<304> 65  
<305> 11  
<306> 4476-  
<307> (1997)

<400> 36  
Asp Ile Leu Lys Val Ile Val Asp Ser Met Asn His His Gly Asp Ala  
1 5 10 15

Arg Ser Lys Leu Arg Glu Glu Leu Ala Glu Leu Thr Ala Glu Leu Lys  
20 25 30

Ile Tyr Ser Val Ile Gln Ala Glu Ile Asn Lys His Leu Ser Ser Ser  
35 40 45

Gly Thr Ile Asn Ile His Asp Lys Ser Ile Asn Leu Met Asp Lys Asn  
50 55 60

Leu Tyr Gly Tyr Thr Asp Glu Glu Ile Phe Lys Ala Ser Ala Glu Tyr  
65 70 75 80

Lys Ile Leu Glu Lys Met Pro Gln Thr Thr Ile Gln Val Asp Gly Ser  
85 90 95

Glu Lys Lys Ile Val Ser Ile Lys Asp Phe Leu Gly Ser Glu Asn Lys  
100 105 110

Arg Thr Gly Ala Leu Gly Asn Leu Lys Asn Ser Tyr Ser Tyr Asn Lys  
115 120 125

Asp Asn Asn Glu Leu Ser His Phe Ala Thr Thr Cys Ser Asp  
130 135 140

<210> 37

<211> 19

<212> PRT

<213> Haemophilus influenzae

<300>

<310> EP-0 432 220-B1

<400> 37

Cys Ser Ser Ser Asn Asn Asp Ala Ala Gly Asn Gly Ala Ala Gln Phe  
1 5 10 15

Gly Gly Tyr

<210> 38

<211> 11

<212> PRT

<213> Haemophilus influenzae

<300>

<310> EP-0 432 220-B1

<400> 38

Asn Lys Leu Gly Thr Val Ser Tyr Gly Glu Glu  
1 5 10

<210> 39

<211> 16

<212> PRT

<213> Haemophilus influenzae

<300>

<310> EP-0 432 220-B1

<400> 39

Asn Asp Glu Ala Ala Tyr Ser Lys Asn Arg Arg Ala Val Leu Ala Tyr  
1 5 10 15

<210> 40

<211> 28

&lt;212&gt; PRT

&lt;213&gt; Moraxella catarrhalis

&lt;300&gt;

&lt;310&gt; WO 98/06851

&lt;400&gt; 40

Leu Asp Ile Glu Lys Asp Lys Lys Lys Arg Thr Asp Glu Gln Leu Gln  
1 5 10 15

Ala Glu Leu Asp Asp Lys Tyr Ala Gly Lys Gly Tyr  
20 25

&lt;210&gt; 41

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Moraxella catarrhalis

&lt;300&gt;

&lt;310&gt; WO 98/06851

&lt;400&gt; 41

Leu Asp Ile Glu Lys Asn Lys Lys Lys Arg Thr Glu Ala Glu Leu Gln  
1 5 10 15

Ala Glu Leu Asp Asp Lys Tyr Ala Gly Lys Gly Tyr  
20 25

&lt;210&gt; 42

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Moraxella catarrhalis

&lt;300&gt;

&lt;310&gt; WO 98/06851

&lt;400&gt; 42

Ile Asp Ile Glu Lys Lys Gly Lys Ile Arg Thr Glu Ala Glu Leu Leu  
1 5 10 15

Ala Glu Leu Asn Lys Asp Tyr Pro Gly Gln Gly Tyr  
20 25

&lt;210&gt; 43

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Porphyromonas gingivalis

&lt;300&gt;

&lt;304&gt; 110

&lt;305&gt; 2

&lt;306&gt; 285-

&lt;307&gt; 1997

&lt;400&gt; 43

Gly Val Ser Pro Lys Val Cys Lys Asp Val Thr Val Glu Gly Ser Asn  
1 5 10 15

Glu Phe Ala Pro Val Gln Asn Leu Thr  
20 25

&lt;210&gt; 44

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Porphyromonas gingivalis

&lt;300&gt;

&lt;304&gt; 110

&lt;305&gt; 2

&lt;306&gt; 285-

&lt;307&gt; 1997

&lt;400&gt; 44

Arg Ile Gln Ser Thr Trp Arg Gln Lys Thr Val Asp Leu Pro Ala Gly  
1 5 10 15

Thr Lys Tyr Val  
20

&lt;210&gt; 45

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Trypanosoma cruzi

&lt;300&gt;

&lt;304&gt; 159

&lt;305&gt; 9

&lt;306&gt; 4444-

&lt;307&gt; (1997)

&lt;400&gt; 45

Ser His Asn Phe Thr Leu Val Ala Ser Val Ile Ile Glu Ala Pro Ser  
1 5 10 15

Gly Asn Thr Cys  
20

<210> 46  
<211> 21  
<212> PRT  
<213> Trypanosoma cruzi

<300>  
<310> WO 97/18475

<400> 46  
Lys Ala Ala Ile Ala Pro Ala Lys Ala Ala Ala Ala Pro Ala Lys Ala  
1 5 10 15

Ala Thr Ala Pro Ala  
20

<210> 47  
<211> 16  
<212> PRT  
<213> Plasmodium falciparum

<300>  
<303> Int. Arch. Allergy Appl. Immunol.  
<304> 114  
<305> 1  
<306> 15-

<400> 47  
Ser Val Gln Ile Pro Lys Val Pro Tyr Pro Asn Gly Ile Val Tyr Cys  
1 5 10 15

<210> 48  
<211> 16  
<212> PRT  
<213> Plasmodium falciparum

<300>  
<303> Int. Arch. Allergy Appl. Immunol.  
<304> 114  
<305> 1



<306> 15-

<400> 48

Asp Phe Asn His Tyr Tyr Thr Leu Lys Thr Gly Leu Glu Ala Asp Cys  
1 5 10 15

<210> 49

<211> 16

<212> PRT

<213> Streptococcus sobrinus

<300>

<303> Arch. Oral Biol.

<304> 35

<306> Suppl. 475-

<307> (1990)

<400> 49

Lys Pro Arg Pro Ile Tyr Glu Ala Lys Leu Ala Gln Asn Gln Lys Cys  
1 5 10 15

<210> 50

<211> 17

<212> PRT

<213> Streptococcus sobrinus

<300>

<303> Arch. Oral Biol.

<304> 35

<306> Suppl. 475-

<307> (1990)

<400> 50

Ala Lys Ala Asp Tyr Glu Ala Lys Leu Ala Gln Tyr Glu Lys Asp Leu  
1 5 10 15

Cys

<210> 51

<211> 16

<212> PRT

<213> Lymphocytic choriomeningitis virus

<300>

<303> Proc. Natl. Acad. Sci. U.S.A.

<304> 94

<305> 7

<306> 3314-

<307> (1997)

<400> 51

Arg Pro Gln Ala Ser Gly Val Tyr Met Gly Asn Leu Thr Ala Gln Cys  
1 5 10 15

<210> 52

<211> 9

<212> PRT

<213> *Shigella flexneri*

<300>

<303> J. Biol. Chem.

<304> 271

<305> 52

<306> 33670-

<307> (1996)

<400> 52

Lys Asp Arg Thr Leu Ile Glu Gln Lys  
1 5

<210> 53

<211> 15

<212> PRT

<213> respiratory syncytial virus

<300>

<304> 234

<305> 1

<306> 118-

<307> 1997

<400> 53

Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys  
1 5 10 15

<210> 54

<211> 19

<212> PRT

<213> *Plasmodium vivax*

&lt;300&gt;

&lt;303&gt; Vaccine

&lt;304&gt; 15

&lt;305&gt; 4

&lt;306&gt; 377-

&lt;307&gt; 1997

&lt;400&gt; 54

Gly Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln  
1 5 10 15

Pro Ala Gly

&lt;210&gt; 55

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Clostridium tetani

&lt;300&gt;

&lt;303&gt; Vaccine

&lt;304&gt; 15

&lt;305&gt; 4

&lt;306&gt; 377-

&lt;307&gt; 1997

&lt;400&gt; 55

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Cys  
1 5 10 15

&lt;210&gt; 56

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Entamoeba histolytica

&lt;300&gt;

&lt;303&gt; J. Exp. Med.

&lt;304&gt; 185

&lt;305&gt; 10

&lt;306&gt; 1793-

&lt;307&gt; 1997

&lt;400&gt; 56

Val Glu Cys Ala Ser Thr Val Cys Gln Asn Asp Asn Ser Cys Pro Ile  
1 5 10 15

Ile Ala Asp Val Glu Lys Cys Asn Gln  
                   20                  25

<210> 57  
 <211> 34  
 <212> PRT  
 <213> Schistosoma japonicum

<300>  
 <303> Vaccine  
 <304> 15  
 <305> 1  
 <306> 79-  
 <307> 1997

<400> 57  
 Asp Leu Gln Ser Glu Ile Ser Leu Ser Leu Glu Asn Gly Glu Leu Ile  
       1                  5                  10                  15

Arg Arg Ala Lys Ser Ala Glu Ser Leu Ala Ser Glu Leu Gln Arg Arg  
                   20                  25                  30

Val Asp

<210> 58  
 <211> 34  
 <212> PRT  
 <213> Schistosoma mansoni

<300>  
 <303> Vaccine  
 <304> 15  
 <305> 1  
 <306> 79-  
 <307> 1997

<400> 58  
 Asp Leu Gln Ser Glu Ile Ser Leu Ser Leu Glu Asn Ser Glu Leu Ile  
       1                  5                  10                  15

Arg Arg Ala Lys Ala Ala Glu Ser Leu Ala Ser Asp Leu Gln Arg Arg  
                   20                  25                  30

Val Asp

<210> 59  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: MseI  
restriction endonuclease site inserted into wild  
type Hepatitis B sequence at position 75

<220>  
<221> CDS  
<222> (1)..(63)

<400> 59  
gct acc tgg gtg ggt gtt aat ttg gaa gat cca gcg tct aga gac cta 48  
Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu  
1 5 10 15  
  
gta gtc agt tat gtc 63  
Val Val Ser Tyr Val  
20

<210> 60  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<400> 60  
Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu  
1 5 10 15  
  
Val Val Ser Tyr Val  
20

<210> 61  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: K inserted at  
amino acid position 75 of Hetatitits B core

## sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(39)

&lt;400&gt; 61

gct acc tgg gtg ggt gtt aaa aat ttg gaa gat cca gcg tc

41

Ala Thr Trp Val Gly Val Lys Asn Leu Glu Asp Pro Ala

1

5

10

&lt;210&gt; 62

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 62

Ala Thr Trp Val Gly Val Lys Asn Leu Glu Asp Pro Ala

1

5

10

&lt;210&gt; 63

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: K inserted at  
amino acid position 76 of hepatitis B core

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3)..(26)

&lt;400&gt; 63

tt aat aaa ttg gaa gat cca gcg tct a

27

Asn Lys Leu Glu Asp Pro Ala Ser

1

5

&lt;210&gt; 64

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 64

Asn Lys Leu Glu Asp Pro Ala Ser

1

5

&lt;210&gt; 65

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: K inserted at  
position 77 of hepatitis B virus core

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3) .. (26)

&lt;400&gt; 65

tt aat ttg aaa gaa gat cca gcg tct a

27

Asn Leu Lys Glu Asp Pro Ala Ser

1

5

&lt;210&gt; 66

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 66

Asn Leu Lys Glu Asp Pro Ala Ser

1

5

&lt;210&gt; 67

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: K inserted at  
position 78 of hepatitis B core

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3) .. (32)

&lt;400&gt; 67

tt aat ttg gaa aaa gat cca gcg tct aga gac

32

Asn Leu Glu Lys Asp Pro Ala Ser Arg Asp

1 5 10

<210> 68  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<400> 68  
Asn Leu Glu Lys Asp Pro Ala Ser Arg Asp  
1 5 10

<210> 69  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: K inserted at  
amino acid position 79 of hepatitis B core

<220>  
<221> CDS  
<222> (3)..(35)

<400> 69  
tt aat ttg gaa gat aaa cca gcg tct aga gac cta g 36  
Asn Leu Glu Asp Lys Pro Ala Ser Arg Asp Leu  
1 5 10

<210> 70  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<400> 70  
Asn Leu Glu Asp Lys Pro Ala Ser Arg Asp Leu  
1 5 10

<210> 71  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: K inserted at  
amino acid position 80 of hepatitis B core

<220>

<221> CDS

<222> (3)..(38)

<400> 71

tt aat ttg gaa gat cca aaa gcg tct aga gac cta gta g

39

Asn Leu Glu Asp Pro Lys Ala Ser Arg Asp Leu Val

1

5

10

<210> 72

<211> 12

<212> PRT

<213> Artificial Sequence

<400> 72

Asn Leu Glu Asp Pro Lys Ala Ser Arg Asp Leu Val

1

5

10

<210> 73

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K inserted at  
amino acid position 81 of hepatitis B core

<220>

<221> CDS

<222> (3)..(41)

<400> 73

tt aat ttg gaa gat cca gcg aaa tct aga gac cta gta gtc ag

43

Asn Leu Glu Asp Pro Ala Lys Ser Arg Asp Leu Val Val

1

5

10

<210> 74

<211> 13

<212> PRT

<213> Artificial Sequence

<400> 74

Asn Leu Glu Asp Pro Ala Lys Ser Arg Asp Leu Val Val  
1 5 10

<210> 75

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K inserted at  
amino acid position 82 of hepatitis B core

<220>

<221> CDS

<222> (3) .. (44)

<400> 75

tt aat ttg gaa gat cca gcg tct aaa aga gac cta gta gtc agt t 45  
Asn Leu Glu Asp Pro Ala Ser Lys Arg Asp Leu Val Val Ser  
1 5 10

<210> 76

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 76

Asn Leu Glu Asp Pro Ala Ser Lys Arg Asp Leu Val Val Ser  
1 5 10

<210> 77

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K inserted at  
amino acid position 83 of hepatitis B core

<220>

<221> CDS

<222> (3) .. (50)

<400> 77

tt aat ttg gaa gat cca gcg tct aga aaa gac cta gta gtc agt tat 47

Asn Leu Glu Asp Pro Ala Ser Arg Lys Asp Leu Val Val Ser Tyr  
 1 5 10 15

gtc 50  
 Val

<210> 78  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<400> 78  
 Asn Leu Glu Asp Pro Ala Ser Arg Lys Asp Leu Val Val Ser Tyr Val  
 1 5 10 15

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: K inserted at  
 amino acid position 84 of hepatitis B core

<220>  
 <221> CDS  
 <222> (3)..(50)

<400> 79  
 tt aat ttg gaa gat cca gcg tct aga gac aaa cta gta gtc agt tat 47  
 Asn Leu Glu Asp Pro Ala Ser Arg Asp Lys Leu Val Val Ser Tyr  
 1 5 10 15

gtc 50  
 Val

<210> 80  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<400> 80  
 Asn Leu Glu Asp Pro Ala Ser Arg Asp Lys Leu Val Val Ser Tyr Val  
 1 5 10 15

<210> 81  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: K inserted at  
amino acid position 85 of hepatitis B core

<220>  
<221> CDS  
<222> (2) .. (31)

<400> 81  
c tcg aga gac cta aaa gta gtc agt tat gtc 31  
Ser Arg Asp Leu Lys Val Val Ser Tyr Val  
1 5 10

<210> 82  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<400> 82  
Ser Arg Asp Leu Lys Val Val Ser Tyr Val  
1 5 10

<210> 83  
<211> 18  
<212> PRT  
<213> Plasmodium vivax

<400> 83  
Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro  
1 5 10 15

Ala Gly

<210> 84  
<211> 8  
<212> PRT  
<213> Influenza virus

&lt;400&gt; 84

Cys Asn Asn Pro His Arg Ile Leu

1

5

&lt;210&gt; 85

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Influenza virus

&lt;400&gt; 85

Cys Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Gly Met

1

5

10

15

Arg Asn Val Pro Glu Lys Gln Thr Arg

20

25

&lt;210&gt; 86

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 86

Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val

1

5

10

15

&lt;210&gt; 87

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 87

Leu Leu Val Ser Ser Lys Val Ser Thr Val Lys Asp Leu Leu Pro

1

5

10

15

&lt;210&gt; 88

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 88

Leu Leu Pro Leu Leu Glu Lys Val Ile Gly Ala Gly Lys Pro Leu

1

5

10

15

<210> 89  
<211> 15  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 89  
Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly Leu  
1 5 10 15

<210> 90  
<211> 15  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 90  
Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys  
1 5 10 15

<210> 91  
<211> 18  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 91  
Ala Arg Arg Gly Leu Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val  
1 5 10 15

Lys Val

<210> 92  
<211> 14  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 92  
Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys  
1 5 10

<210> 93  
<211> 17  
<212> PRT  
<213> Mycobacterium tuberculosis

&lt;400&gt; 93

Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu Thr  
1 5 10 15

Leu

&lt;210&gt; 94

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Mycobacterium tuberculosis

&lt;400&gt; 94

Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val Glu Glu Gly  
1 5 10 15

&lt;210&gt; 95

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 95

Cys Asp Ile Ile Gly Asn Thr Trp Asn Pro Ser Asp Gln Glu Pro Phe  
1 5 10 15

Pro Gly Tyr Gly  
20

&lt;210&gt; 96

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 96

Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Glu Thr  
1 5 10 15

Gln Gln Gly His Thr  
20

&lt;210&gt; 97

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 97

Gly Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys  
1 5 10

&lt;210&gt; 98

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 98

Thr Asp Ile Gln Ala Leu Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser  
1 5 10 15

Leu Thr Ser Leu Ser Glu  
20

&lt;210&gt; 99

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 99

Ala Lys Leu Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe  
1 5 10

&lt;210&gt; 100

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 100

Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp  
1 5 10 15

Phe Thr Thr Leu Ile Ser Ser  
20

&lt;210&gt; 101

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Feline leukemia virus

&lt;400&gt; 101



Gln Val Met Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn Leu Val  
1 5 10 15

Leu Pro

<210> 102  
<211> 17  
<212> PRT  
<213> Feline leukemia virus

<400> 102  
Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Ile Glu Ser Arg Val Thr  
1 5 10 15

Pro

<210> 103  
<211> 15  
<212> PRT  
<213> Feline leukemia virus

<400> 103  
Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly Gly Leu Cys  
1 5 10 15

<210> 104  
<211> 25  
<212> PRT  
<213> Feline leukemia virus

<400> 104  
Gln Glu Gly Gly Leu Cys Ala Ala Leu Glu Glu Cys Gln Ile Gly Gly  
1 5 10 15

Leu Cys Ala Ala Leu Lys Glu Glu Cys  
20 25

<210> 105  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<300>

<303> Science

<304> 228

<306> 1436-1440

<307> 1985

<400> 105

Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro  
1 5 10

<210> 106

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 106

Cys Met Gln Leu Arg Ser  
1 5

<210> 107

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 107

Cys Arg Phe Ser Ile Asn  
1 5

<210> 108

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 108

Cys Ala Val Pro Arg  
1 5

<210> 109

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 109

Cys Ile Pro Arg Ser  
1 5

<210> 110

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 110

Cys Phe Ile Pro Val  
1 5

<210> 111

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

<400> 111

Cys Thr Val Ser Gly Ala

1

5

&lt;210&gt; 112

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Cytochrome  
P-450 fragment

&lt;400&gt; 112

Cys Thr Leu Ser Gly Glu

1

5

&lt;210&gt; 113

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Plasmodium knowlesi

&lt;400&gt; 113

Gln Ala Gln Gly Asp Gly Ala Asn Ala Gly Gln Pro

1

5

10

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/03055

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A61K39/00, 39/38, 39/29; C07K 7/00, 15/00

US CL : 424/184.1, 189.1; 530/324, 325, 326; 536/23.72

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/184.1, 189.1; 530/324, 325, 326; 536/23.72

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, APS, CAS ONLINE

search terms: hepatitis B, core protein, hapten, fusio?, pendent?, antigenic, Ab, immunoglo?, antibodies.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOLETZKI et al. Mosaic hepatitis B virus core particles allow insertion of extended foreign protein segments. Journal of General Virology. 1997, Vol. 78, pages 2049-2053, see the entire document.	1-22
Y	SHIAU et al. Mutated Epitopes of Hepatitis B Surface Antigen Fused to the Core Antigen of the Virus Induce Antibodies That React With the Native Surface Antigen. Journal of Medical Virology. 1997, Vol. 51, pages 159-166, see the entire document.	1-22
Y	US 5,143,726 A (THORNTON et al) 01 September 1992, see the claims.	1-22
Y	US 4,818,527 A ( THORNTON et al) 04 April 1989, see the claims	1-22



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

Date of mailing of the international search report

20 MAY, 1999

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No.

Authorized officer

Telephone No.

**INTERNATIONAL SEARCH REPORT**International application No.  
PCT/US99/03055**C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 4,882,145 A (THORNTON et al ) 21 November 1989, see the claims.	1-22
A,E	US 5,840,303 A (CHISARI et al) 24 November 1998, see the abstract, and the claims.	1-22

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/03055

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/03055

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

Group I, claim(s) 1-7, drawn to hepatitis B core protein conjugated to a hapten wherein hapten is pendently linked wherein hepatitis protein is identified with a specific sequence.

Group II, claim(s) 8, drawn to hepatitis B core protein particles comprising an insert that is antigenic.

Group III, claim(s) 9-13, drawn to hepatitis B core protein pendently linked to a hapten .

Group IV, claim(s) 14, 15, drawn to an immunogenic fusion protein conjugated to hapten pendently linked to three peptide domains of hepatitis B core protein.

Group V, claim(s) 16, drawn to hepatitis B core protein particles comprising an insert that is non-antigenic.

Group VI, claim(s) 17-19, drawn to a vaccine composition of hepatitis B core protein and a hapten.

Group VII, claim(s) 20-22, drawn to process of inducing antibodies against hepatitis B core protein and hapten.

The inventions listed as Groups I-VII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I and II-VII are directed to different sets of hepatitis B core proteins with different hapten(s) and multitude of different characteristics, different sets of nucleotide and domains, that are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept, accordingly, the unity of invention is lacking among the groups.